Notch3 Is Necessary for Blood Vessel Integrity in the Central Nervous System

Henshall, T L ; Keller, A ; He, L ; Johansson, B R ; Wallgard, E ; Raschperger, E ; Mae, M A ; Jin, S ; Betsholtz, C ; Lendahl, U

DOI: https://doi.org/10.1161/ATVBAHA.114.304849

Notch3 Is Necessary for Blood Vessel Integrity in the Central Nervous System

Tanya L. Henshall,* Annika Keller,* Liqun He, Bengt R. Johansson, Elisabet Wallgard, Elisabeth Raschperger, Maarja Andaloussi Mäe, Shaobo Jin, Christer Betsholtz,† Urban Lendahl†

Objective—Vascular smooth muscle cells (VSMC) are important for contraction, blood flow distribution, and regulation of blood vessel diameter, but to what extent they contribute to the integrity of blood vessels and blood–brain barrier function is less well understood. In this report, we explored the impact of the loss of VSMC in the *Notch3*$^{-/-}$ mouse on blood vessel integrity in the central nervous system.

Approach and Results—*Notch3*$^{-/-}$ mice showed focal disruptions of the blood–brain barrier demonstrated by extravasation of tracers accompanied by fibrin deposition in the retinal vasculature. This blood–brain barrier leakage was accompanied by a regionalized and patchy loss of VSMC, with VSMC gaps predominantly in arterial resistance vessels of larger caliber. The loss of VSMC appeared to be caused by progressive degeneration of VSMC resulting in a gradual loss of VSMC marker expression and a progressive acquisition of an aberrant VSMC phenotype closer to the gaps, followed by enhanced apoptosis and cellular disintegration in the gaps. Arterial VSMC were the only mural cell type that was morphologically affected, despite Notch3 also being expressed in pericytes. Transcriptome analysis of isolated brain microvessels revealed gene expression changes in *Notch3*$^{-/-}$ mice consistent with loss of arterial VSMC and presumably secondary transcriptional changes were observed in endothelial genes, which may explain the compromised vascular integrity.

Conclusions—We demonstrate that Notch3 is important for survival of VSMC, and reveal a critical role for Notch3 and VSMC in blood vessel integrity and blood–brain barrier function in the mammalian vasculature. **(*Arterioscler Thromb Vasc Biol*. 2015;35:409-420. DOI: 10.1161/ATVBAHA.114.304849.)**

Key Words: aneurysm ■ blood-brain barrier ■ fibrin ■ Notch3 ■ smooth muscle

All blood vessels are composed of 2 principal cell types, endothelial cells and mural cells (vascular smooth muscle cells [VSMC] and pericytes). Mural cells have different phenotypic and functional characteristics, depending on the type of blood vessel. For example, VSMC in certain types of arteries are important regulators of vessel tone and diameter, while in large caliber vessels, VSMC contribute critical extracellular matrix components.[1] The function of capillary pericytes, however, is just beginning to emerge.[2] A role for pericytes at the blood–brain barrier (BBB) was recently demonstrated through analysis of mice mutated in the genes, *Pdgfb* and *Pdgfrb*, encoding platelet-derived growth factor-B and its receptor, PDGF-B and PDGFR-β, respectively.[3,4] In these mice, loss of pericytes led to increased endothelial transcytosis and a significant transport of blood-borne tracers, including large proteins, across the normally restrictive BBB.[3,4] To what extent the mural cells of larger vessels are also critical for the integrity of the BBB is unknown. In this study, we have used *Notch3*$^{-/-}$ mice to address this question, as these mice show progressive loss of arterial VSMC over time.[5–7]

Notch signaling is an evolutionarily conserved cell–cell signaling mechanism based on interactions between transmembrane Notch receptors and Delta/Jagged ligands on juxtaposed cells. Signaling ensues when a ligand on the signal-sending cell interacts with a Notch receptor on the neighboring signal-receiving cell. Ligand-receptor interaction leads to proteolytic processing of the Notch receptor, which ultimately releases the intracellular portion of the receptor (Notch intracellular domain). The Notch intracellular domain then translocates to the cell nucleus, where it interacts with the DNA-binding protein, CSL (Cp-binding factor 1 [CBF-1]/recombination signal sequence-binding protein-Jκ [RBP-Jκ], suppressor of hairless

Received on: March 24, 2014; final version accepted on: November 13, 2014.

From the Department of Cell and Molecular Biology (T.H., S.J., U.L.) and Department of Medical Biochemistry and Biophysics, Division of Vascular Biology (C.B., E.R.), Karolinska Institute, Stockholm, Sweden; Department of Immunology, Genetics, and Pathology, Rudbeck Laboratory, Uppsala University, Uppsala, Sweden (A.K., L.H., E.R., M.A.M., C.B.); EM Unit, Institute of Biomedicine, University of Gothenburg, Gothenburg, Sweden (B.R.J.); and Octapharma AB, Stockholm, Sweden (E.W.).

*These authors contributed equally to this article.

†Shared senior authors.

Current address for A.K.: Division of Neurosurgery, University Hospital Zürich, Zürich, Switzerland.

The online-only Data Supplement is available with this article at http://atvb.ahajournals.org/lookup/suppl/doi:10.1161/ATVBAHA.114.304849/-/DC1.

Correspondence to Professor Christer Betsholtz, Department of Medical Biochemistry and Biophysics, Division of Vascular Biology, Uppsala University, 751 85 Uppsala, Sweden. E-mail Christer.Betsholtz@igp.uu.se; or Professor Urban Lendahl, Department of Cell and Molecular Biology, Karolinska Institute, SE-171 77 Stockholm, Sweden. E-mail Urban.Lendahl@ki.se

Nonstandard Abbreviations and Acronyms

β-gal	β-galactosidase
BBB	blood–brain barrier
CADASIL	cerebral autosomal dominant arteriopathy with subcortical infarcts and leukoencephalopathy
CNS	central nervous system
GOM	granular osmiophilic material
PDGF-B	platelet-derived growth factor-B
SMA	α-smooth muscle actin
TEM	transmission electron microscopy
VSMC	vascular smooth muscle cells

[Su(h)], and Lag-1) and induces transcription of downstream target genes.[8]

Notch signaling plays a pivotal role during vascular development. Genetic targeting of several Notch pathway components in endothelial cells (Notch1, Dll4, RBP-Jκ) leads to severe defects in angiogenic sprouting and vessel remodeling.[9,10] The Notch3 receptor is closely related to Notch1, 2, and 4[11,12] and is expressed in VSMC. Upregulation of human *NOTCH3* as a consequence of hypoxia is observed in VSMC in pulmonary arterial hypertension, and reduction of Notch3 signaling mitigates pathogenesis of pulmonary arterial hypertension in mice.[13] Mutations in the *NOTCH3* gene are the cause of cerebral autosomal dominant arteriopathy with subcortical infarcts and leukoencephalopathy (CADASIL),[14] the most common inherited stroke and dementia syndrome in the group of degenerative small vessel diseases.[15] In patients with CADASIL, VSMC degenerate over time and an electron-dense extracellular material, granular osmiophilic material (GOM) is deposited.[16] It has been proposed that the formation of GOM around VSMC is central to the disease process,[17] although deregulation of the Notch signaling output per se as a result of CADASIL mutations cannot be excluded.[18,19] Mouse models overexpressing Notch3 with CADASIL mutations recapitulate certain aspects of the disease, including the generation of GOM.[19–21] *Notch3*$^{-/-}$ mice are viable and fertile but exhibit a progressive loss of VSMC after an initially normal vascular development and do not produce GOM.[5–7] Reduced *Pdgfrb* expression has been observed in *Notch3*$^{-/-}$ mice at P0,[6] and a vascular phenotype in the retina is observed from P3 characterized by delayed angiogenesis early in development and loss of VSMC around developing retinal arteries.[7] The *Notch3*$^{-/-}$ VSMC phenotype leads to an altered myotonic tone[5,22] and the *Notch3*$^{-/-}$ mice are also more susceptible to experimental ischemic stroke.[23]

In this report, we explored whether VSMC are important for vascular integrity using the *Notch3*$^{-/-}$ mouse as a model. We show that loss of VSMC in *Notch3*$^{-/-}$ mice occurs by a slow, continuous rate of apoptosis, and in adult mice is linked to localized impairment of the BBB and an intra-arterial accumulation of fibrin. This demonstrates that gradual erosion of the VSMC coat affects vessel integrity in the central nervous system (CNS).

Materials and Methods

Materials and Methods are available in the online-only Data Supplement.

Results

Gaps in SMA Staining in *Notch3*$^{-/-}$ Mice Correlate With Vessel Type and Size

To gain better insights into the *Notch3*$^{-/-}$ vascular phenotype, we first wanted to establish whether VSMC alterations in adult *Notch3*$^{-/-}$ mice were confined to vessels of a specific type and size. To address this, we searched for mural cell phenotypes in the retina of adult *Notch3*$^{-/-}$ mice, a structure with a highly visible vascular tree: primary arterioles radiate out of the optic nerve head and stretch across the retinal inner surface while undergoing progressive branching. We found patchy loss of expression of α-smooth muscle actin (SMA; a VSMC marker) along retinal arterioles leaving apparent gaps in the SMA-positive VSMC coat adjacent to regions with sparse and irregular SMA staining (Figure 1A), in agreement with previously published work.[7] Extensive loss of SMA staining was observed along the *Notch3*$^{-/-}$ primary radial arterioles (Figure 1B; boxed area), and the SMA loss was then quantified along the proximodistal arterial axis of these vessels. When scoring arterioles in the central (0–820 μm), middle (820–1640 μm), and peripheral (1640–2710 μm) portions of the retina (Figure 1C), SMA loss was predominantly observed in the central and middle regions, whereas the distal region was largely preserved (Figure 1D). The arteriolar branching pattern showed no significant difference between the different genotypes (Figure I in the online-only Data Supplement), in agreement with a recent report.[7] Loss of VSMC coverage appeared specific to arterioles, as we could not detect similar changes in venules (Figure II in the online-only Data Supplement).

In the adult *Notch3*$^{-/-}$ mouse, SMA gaps were also observed in brain arteries (Figure III in the online-only Data Supplement). The brain receives its arterial blood supply from the anterior, middle, and posterior cerebral arteries extending off the Circle of Willis. These arteries ramify in the pia and penetrate perpendicularly into the brain parenchyma, where they further divide into smaller diameter parenchymal arterioles (schematized in Figure IIIA in the online-only Data Supplement). Upon analysis of the cerebral vasculature of adult *Notch3*$^{-/-}$ mice, we found distinct gaps in SMA staining in pial and penetrating branches, whereas smaller caliber parenchymal arterioles showed little or no loss of SMA staining (Figure IIIB in the online-only Data Supplement). Based on these observations, we conclude that SMA gaps are primarily associated with arterial resistance vessels of larger caliber both in the retina and in the brain.

Progressive Loss of VSMC in the *Notch3*$^{-/-}$ Vasculature

We next asked whether the observed phenotype was caused by a gradual or more abrupt loss of VSMC. Retinal arterial SMA staining in *Notch3*$^{-/-}$ mice was sparser than in controls already by postnatal day (P) 10 (Figure IV in the online-only Data Supplement). Apparent gaps in the VSMC coverage were, however, evident by P20 (Figure IV in the online-only Data Supplement) and prominent by 6 months, at which time ≤40% of SMA staining was lost (Figure 1D). Focusing on the gaps in SMA expression, we immunostained for additional mural cell

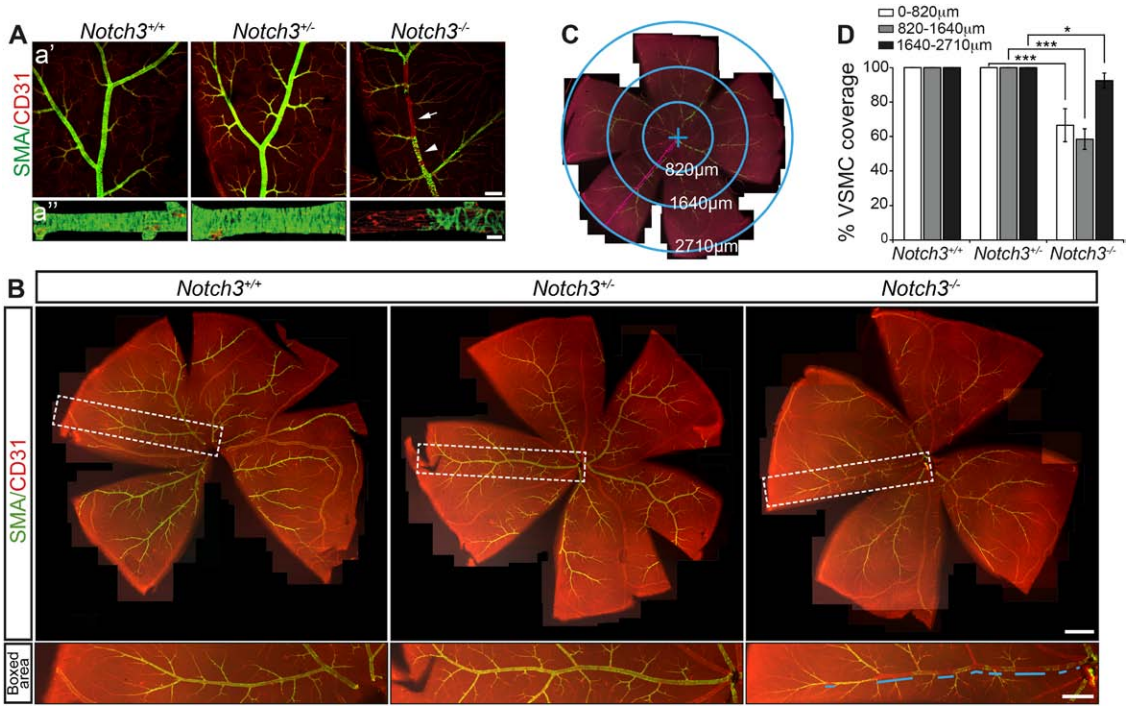


Figure 1. Gaps in α-smooth muscle actin (SMA) staining correlate with vessel type and size in the *Notch3*$^{-/-}$ retina. **A**, SMA and CD31 staining of adult *Notch3*$^{+/+}$, *Notch3*$^{+/-}$,and *Notch3*$^{-/-}$ mouse retinas in low (**a**′) and high (**a**′′) magnification. Arrow indicates gaps in vascular smooth cells (VSMC) coverage and arrowhead shows disrupted VSMC coverage. **B**, Composite images of retinal vasculature (VSMC in green and endothelium in red) covering the entire adult retina. Images were stitched and blended together using Adobe Photoshop CS6 automatic image merge function (see Methods in online-only Data Supplement). The boxed area shows one representative primary radial arteriole taken from the larger image, above. Blue lines highlight the location of gaps in VSMC coverage. **C**, Retina with overlaid scale bar used to divide the retina into 3 zones for quantification. **D**, Quantification of VSMC coverage in 3 zones along the primary arterioles in the retina. Data are presented as mean±SD. **D**, n=4 per genotype. Scale bars: **a**′, 100 μm; **a**′′, 20 μm; **B**, 400 μm; **B** (boxed area), 200 μm. **P*<0.05; ****P*<0.005.

markers and found that some regions still retained expression of desmin, NG2, and β-galactosidase (β-gal) immunoreactivity (resulting from β-gal expression from the lacZ gene that was knocked into the Notch3 locus[24]; see also below, Figures 4 and 2A–2C). In addition, regions of weak SMA staining were also evident, particularly at the border of gaps (Figure V in the online-only Data Supplement).

The apparent gradual loss of arterial SMA expression and the partial retention of other VSMC markers (desmin, NG2 and β-gal) in *Notch3*$^{-/-}$ mice is consistent with either of 2 scenarios: (1) a switch in the VSMC phenotype with retained cell viability, leading to a progressive loss of VSMC markers, or (2) a degenerative process leading to cell death during which different VSMC proteins degrade at different rates. To distinguish between these alternatives, we used transmission electron microscopy (TEM) to analyze the VSMC phenotype at higher resolution. We first focused on analyzing the region located between normal-looking VSMC and the gaps in the SMA staining, reasoning that those intermediate areas may constitute a zone where progressive degradation of VSMC could be studied. Close to the gaps, the morphology of VSMC appeared altered (Figure 2A) and to capture transitions between the intact VSMC coat and gaps, we studied longitudinally sectioned primary radial arteriolar branches by TEM. In *Notch3*$^{+/-}$ mice, a single continuous layer of basement membrane–embedded VSMC constituted the mural coat of these vessels (Figure 2D). VSMC located in this intermediate zone had a distinctive ultrastructural phenotype, including transversally oriented mitochondria, dense cytoplasmic microfilaments, and abluminal caveolae (Figure 2E). Figure 2F shows a *Notch3*$^{-/-}$ primary radial arteriolar branch spanning a site progressing from an intact VSMC coat (left) to a gap (right). Here, VSMC with an apparently normal morphology (Figure 2F; left) existed adjacent to cells exhibiting altered morphology, which, in turn, border a gap containing cells at various stages of disintegration (Figure 2F; middle and right). Typical features of the latter include discontinuous plasma membranes, cell fragmentation into membrane-enclosed vesicles of different size and content, and amorphous cellular debris. Importantly, all these structures were trapped within a thickened basement membrane (Figure 2F; right).

We also identified a novel and unexpected phenotype in VSMC across the arterial vasculature both in the retina and the brain (Figure 2G and 2H). The phenotype was characterized by an altered endoplasmatic reticulum morphology of large stacks of folded membranes but without any overt signs of degeneration of the VSMC. The broad distribution, combined with the lack of degeneration, suggests that the endoplasmatic reticulum reorganization may be an early manifestation of Notch3 deficiency and precede more overt morphological changes. Collectively, TEM analysis, in addition to capturing an early VSMC phenotype in the endoplasmatic reticulum, provides strong support that VSMC in *Notch3*$^{-/-}$ mice undergo a stepwise deterioration process involving slow degradation and

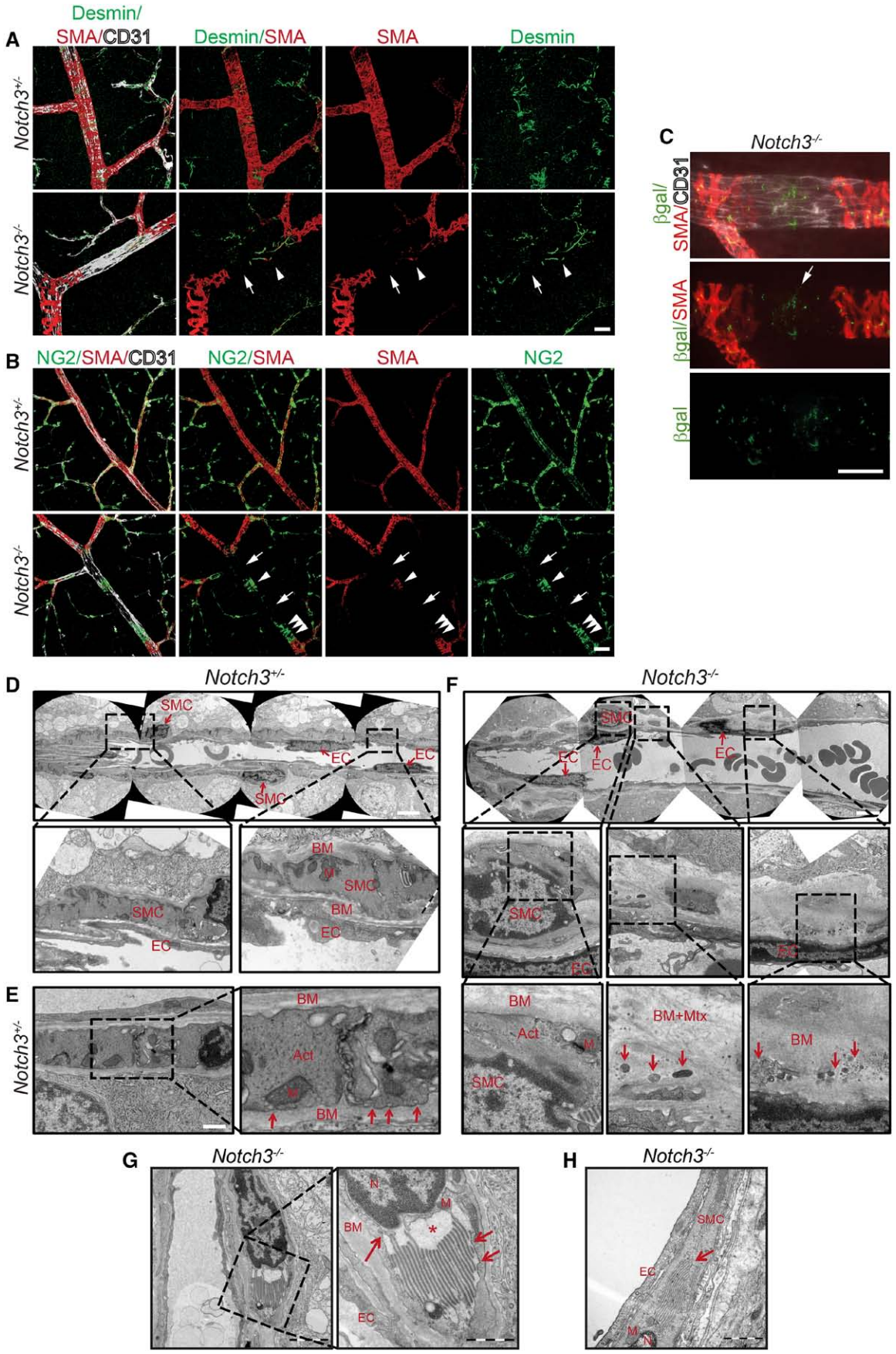


Figure 2. (Continued)

clearance of debris. This is consistent with the gradual disappearance of immunoreactivity for different VSMC markers and is strongly suggestive of degenerative loss of VSMC.

Increased and Localized Apoptosis in *Notch3*$^{-/-}$ VSMC

To gain further insights into the degradation process observed at the TEM level, we explored whether apoptosis was increased in the *Notch3*$^{-/-}$ vasculature by analyzing the number and location of cells with expression of cleaved caspase 3. In wild-type mice (P30), there was a low level of cleaved caspase 3 expression, and the caspase 3-positivity was consistently found in cells located precisely at the branch points along the primary radial arteriole (Figure 3A). The frequency as well as the intensity of cleaved caspase 3-staining in these branch point cells was further enhanced in the *Notch3*$^{-/-}$ retinas (Figure 3A and 3B); however, as in the adult (Figure I in the online-only Data Supplement), no change in the total number of branch points was observed between all genotypes at P30 (Figure 3A and 3B). The level of apoptosis was also increased in *Notch3*$^{-/-}$ retinas in comparison with wild-type controls along straight regions of the radial vessels (not associated with the branch points; Figure 3A and 3B). The frequency of caspase 3-positive cells was even more pronounced in retinas of 9-month-old mice, in which cleaved caspase 3 was also detected within large gaps, along with small traces of SMA from what are presumably dead VSMC (Figure 3C). In conclusion, we thus observed a localized form of apoptosis, which was increased in the *Notch3*$^{-/-}$ vasculature, further supporting the notion that VSMC deteriorate in the *Notch3*$^{-/-}$ vessel wall.

Transcriptome Profiling of Notch3-Deficient Brain Vasculature Reveals Alterations in Markers for VSMC, Pericytes, and Endothelial Cells

To explore further the molecular consequences of Notch3 deficiency and VSMC degeneration, we performed genome-wide transcriptional profiling of brain vasculature, but before the transcriptome analysis, we first wanted to establish in which vascular cell types Notch3 was expressed. To address this, we took advantage of the fact that the *lacZ* reporter gene had been knocked-in into the *Notch3* locus[24] in the *Notch3*$^{+/-}$ and *Notch3*$^{-/-}$ mice, and we therefore used expression of β-gal as a proxy for Notch3 expression.[6] In *Notch3*$^{+/-}$ mice, β-gal immunoreactivity was observed along arterioles, venules, and capillaries in the retina (Figure 4A–4D), and in the brain (Figure VI in the online-only Data Supplement). β-Gal immunoreactivity colocalized with expression of SMA, around arterioles and venules, and the pericyte marker, CD13, along capillaries (Figure 4D). In contrast, no β-gal immunoreactivity was observed in endothelial cells (Figure 4E–4F). High resolution confocal analysis in a segment of *Notch3*$^{+/-}$ brain artery showed Notch3 expression specifically within the SMA-expressing VSMC layer (Figure 4E), while punctate β-gal immunoreactivity adjacent to all VSMC nuclei (Figure 4F) indicated uniform Notch3 expression in brain arterial VSMC. In conclusion, these data show that Notch3 is expressed by all types of vascular mural cells in the CNS but not detectably by endothelial cells.

To assess the vascular transcriptome, vascular fragments, which contain endothelial cells, pericytes, VSMC, and astrocyte end-feet,[3] were isolated from whole brains and then analyzed using Affymetrix expression arrays. A heat map of significantly differentially expressed genes between genotypes and brain regions illustrates clusters of transcripts consistently upregulated or downregulated in *Notch3*$^{-/-}$ vasculature (Figure 4G). In this analysis, cerebral and cerebellar regions were harvested and analyzed separately to identify any regional specific transcriptional changes. The corresponding genes are partially listed in Figure 4H and fully listed in Tables I and II in the online-only Data Supplement. Reassuringly, *Notch3* ranked highest among the downregulated genes and several known Notch target genes (*Hey2*, *Hey-like*, and *Nrarp*) were also significantly and consistently downregulated in the *Notch3*$^{-/-}$ brain vasculature (Figure VII and Table I in the online-only Data Supplement). Of these, Hey-like expression has previously been demonstrated to overlap with Notch3 expression in VSMC in the developing mouse embryo.[25] Also Syndecan-2 was downregulated in *Notch3*$^{-/-}$ vasculature, consistent with a previous report suggesting that Notch3 signaling activates Syndecan-2 expression.[26]

We were primarily interested in expression changes occurring in specific vascular cell populations. The mouse brain endothelial transcriptome has been analyzed,[27] and mural cell gene expression has also been deduced indirectly.[27] Using these data, we classified the transcriptional changes in our data set. Out of 1631 endothelial gene transcripts, 97 (6%) were differentially expressed >1.5-fold

Figure 2 (Continued). Progressive loss of vascular smooth cells (VSMC) marker expression in the *Notch3*$^{-/-}$ retinal vasculature. **A** and **B**, Adult *Notch3*$^{-/-}$ retinas immunostained with antibodies to desmin (**A**) or NG2 (**B**) and costained for α-smooth muscle actin (SMA) immunoreactivity. Arrows point to gaps in mural marker stainings, arrowheads point to cells that have lost or display weak SMA expression but are positive for desmin or NG2. **C**, High magnification view of a retinal arteriole immunostained for β-galactosidase (β-gal), SMA, and CD31. The arrow points to a gap in SMA reactivity along the vessel showing β-gal expression. **D–G**, Transmission electron microscopic (TEM) analysis of retinal arteries. Retinas were flat-mounted and sectioned en face to allow longitudinal sectioning of primary radial branches. **Top** of **D** and **F** show longitudinal sections of a *Notch3*$^{+/-}$ control vessel (**D**) and a *Notch3*$^{-/-}$ vessel (**F**). Note the single, continuous layer of basement membrane (BM)-embedded VSMC in the control. In the *Notch3*$^{-/-}$ vessel, the images capture the transition from an apparently intact VSMC coat (left part of **F**, **top**) to a gap (**F**, middle and right) that contains cells and cellular debris at different degrees of disintegration. **E**, Control VSMC displaying typical ultrastructural features. Arrows in **E** point to abluminal caveolae. Arrows in **F** lower panel insets point to BM-embedded vesicular remnants of disintegrated cells. **G**, TEM images of retinal VSMC reveal expanded stacks of membranes in *Notch3*$^{-/-}$ VSMC. The altered organelles display features characteristic of endoplasmatic reticulum (ER): short arrows point to the outer ER membrane (note ribosomes between the 2 arrows) and the long arrow indicates a point of continuity between the ER and the outer nuclear membrane. The stack of folded membranes is found within a dilated ER cistern (asterisk). **H**, Stacks of folded membranes (arrow) are also seen by TEM analysis of *Notch3*$^{-/-}$ brain VSMC. SMC – smooth muscle cell; EC indicates endothelial cell; M, mitochondria; N, nucleus; Act, actin cytoskeleton; mtx, fibrillar matrix. Scale bars: **A**, 20 μm; **B**, 45 μm; **C**, 40 μm; **D**, 5 mm; **E**, 0.5 μm; **F**, 5 μm; **G**, 2 μm; **H**, 1 μm.

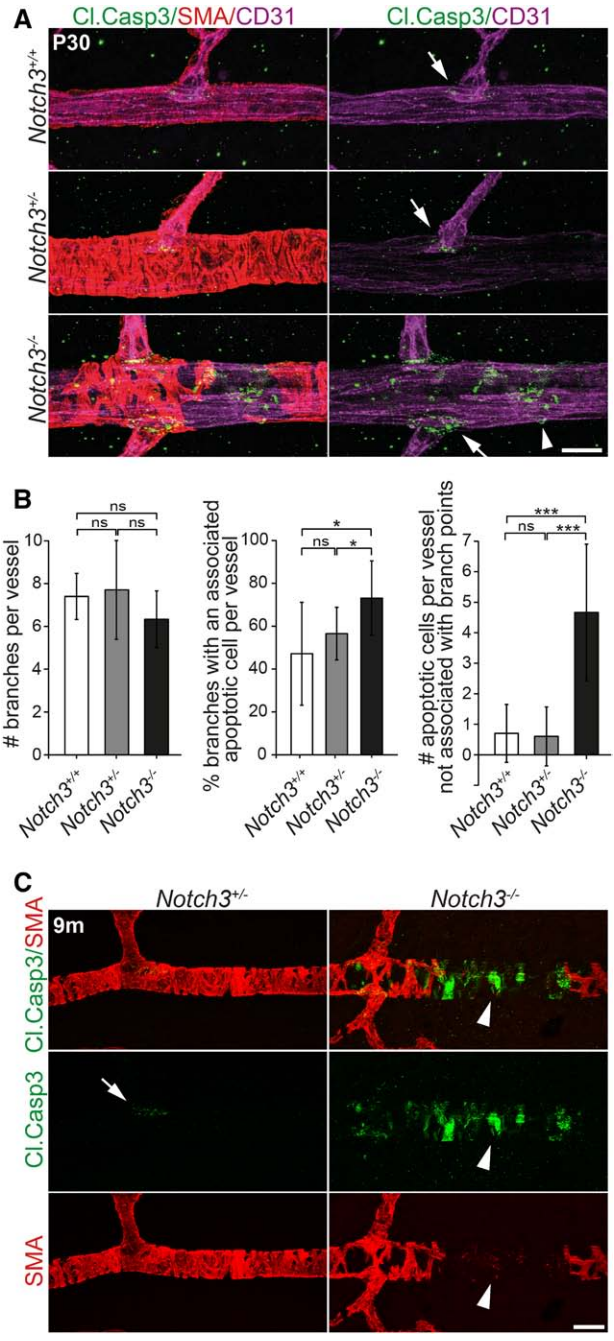


Figure 3. Progressive loss of *Notch3*$^{-/-}$ vascular smooth cells (VSMC) occurs by apoptosis. **A**, Cleaved caspase 3-positive cells (in green) can be seen at branch points (arrows) and along the vessel (arrowhead). **B**, Quantification of vessel branch points, branches with apoptotic cells, and number of apoptotic cells between branches in the first 1200 mm of primary radial arterioles in the retina (P30). Graphs show a significant increase in apoptotic cells along the primary radial arterioles in *Notch3*$^{-/-}$ mice by P30. **C**, Confocal images of primary arterioles in 9-month-old *Notch3*$^{+/-}$ and *Notch3*$^{-/-}$ mice show accumulation of cleaved caspase 3 and α-smooth muscle actin (SMA) in gaps of aged *Notch3*$^{-/-}$ mice (arrowhead). Similar to P30, *Notch3*$^{+/-}$ shows low level apoptosis at the branch points (arrow) at 9 months. **B**, n=3 per genotype. Data are presented as mean±SD. Scale bars: **A**, 20 μm; **C**, 50 μm. *P<0.05; **P<0.01; ***P<0.005.

(32 up and 65 down in *Notch3*$^{-/-}$; Table III in the online-only Data Supplement). Of note, a significantly higher proportion of mural cell gene transcripts were differentially expressed (66 of 175 genes; 38%) and a majority of these (58 genes) were downregulated in *Notch3*$^{-/-}$ (Table IV in the online-only Data Supplement).

Given the expression of Notch3 in pericytes (Figure 4D), we wanted to compare the transcriptome data to data from a mouse model with a severely reduced number of brain pericytes: the PDGF-B retention motif knockout mice (*Pdgfb*$^{ret/ret}$).[3] We found that the overall transcriptome changes observed in *Notch3*$^{-/-}$ vascular fragments were distinct from those observed in *Pdgfb*$^{ret/ret}$ mice. A comparison between the most upregulated and downregulated genes in microvascular fragments from *Notch3*$^{-/-}$ and *Pdgfb*$^{ret/ret}$ mice revealed no apparent similarities (Figure 4H). However, selective analysis of known endothelial and mural cell markers revealed significant downregulation of mural cell markers in both mutants (Figure 4I). Typical pericyte markers were more reduced in *Pdgfb*$^{ret/ret}$ than in *Notch3*$^{-/-}$ mice, whereas typical VSMC markers were similarly reduced. This difference correlates with the strong reduction in pericyte numbers in *Pdgfb*$^{ret/ret}$ mice,[3] whereas both mutants show loss of arterial VSMC. Taken together, the transcriptome analysis of *Notch3*$^{-/-}$ mice is consistent with a selective reduction in the abundance of arterial VSMC accompanied by a smaller change in the transcriptional profile of endothelial cells.

The transcriptional changes in pericyte marker expression in the *Notch3*$^{-/-}$ mice do not prove that pericytes are affected because pericyte markers are also expressed by VSMC (in contrast to VSMC markers, which are not expressed by pericytes). However, the downregulation of pericyte markers in *Notch3*$^{-/-}$ mice, although less dramatic than in the *Pdgfb*$^{ret/ret}$ mice, nevertheless prompted us to more directly assess whether pericytes were morphologically altered in the *Notch3*$^{-/-}$ mice. Pericyte staining with anti-CD13 antibodies revealed normal numbers, distribution, and morphology of CD13-positive cells in both retinal (Figure 4J and 4K and Figure VIII in the online-only Data Supplement) and brain (Figure 4L) capillaries. In addition, capillary density, which is known to be reduced in association with pericyte deficiency,[3,4] was similar in *Notch3*$^{+/-}$ and *Notch3*$^{-/-}$ mice (Figure 4M). This suggests that arterial VSMC, but not pericytes, are morphologically affected by the loss of Notch3.

Reduced Vessel Integrity in the *Notch3*$^{-/-}$ Mouse CNS

Because absence of Notch3 and subsequent VSMC loss provoked transcriptional changes in close to 100 endothelial-associated genes (Table III in the online-only Data Supplement), we asked whether loss of VSMC in the *Notch3*$^{-/-}$ mice would impact on the functional integrity of the CNS vasculature. To assess this, we injected various tracers into the circulation and analyzed potential extravasation into brain and retinal parenchyma. In all *Notch3*$^{-/-}$ brains, but never in controls, we observed sporadic local leakage of Evans blue, which was significant on quantification (Figure 5A and 5B). The same observation was made for horseradish peroxidase (Figure 5C). This type of leakage,

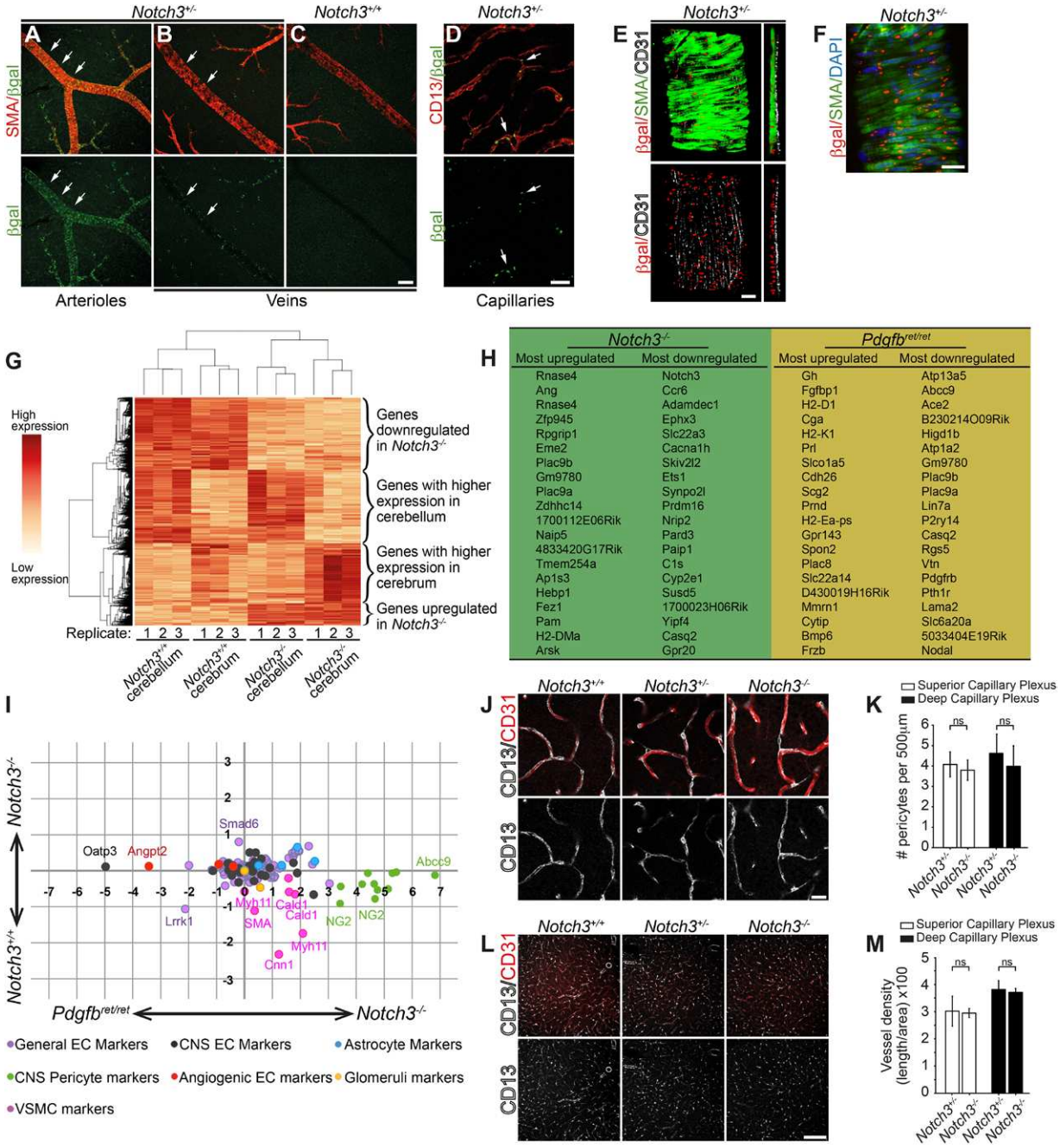


Figure 4. Transcriptome analysis of *Notch3*$^{-/-}$ and *Notch3*$^{+/+}$ microvascular fragments. **A**–**D**, β-Galactosidase (β-gal) immunoreactivity was used as a proxy for Notch3 expression. Confocal images show arterioles (**A**), venules (**B**), and capillaries (**D**) in the adult *Notch3*$^{+/-}$ mouse retina. No β-gal immunoreactivity was observed in the control (*Notch3*$^{+/+}$) retina (**C**). Arrows show β-gal colocalization with the vascular smooth cells (VSMC) marker, α-smooth muscle actin (SMA) along arterioles (**A**) and venules (**B**), and also with the pericyte marker, CD13 along capillaries (**D**). **E** and **F**, Three-dimensional reconstructions of confocal image z-stacks showing a pial brain artery in the adult *Notch3*$^{+/-}$ mouse immnostained for β-gal (in red), SMA (VSMC layer, in green), and CD31 (endothelium, in white). These images demonstrate expression of β-gal (Notch3) specifically within the VSMC layer (**E**), and consistent, punctate β-gal expression around the nuclei (4',6-diamidino-2-phenylindole) of all VSMC (**F**). **G**, Heatmap of differentially expressed genes in *Notch3*$^{+/+}$ and *Notch3*$^{-/-}$ vascular fragments isolated from cerebrum or cerebellum as indicated, in 3 replicates. **H**, Lists of the most highly differentially expressed genes in *Notch3*$^{-/-}$ brain vasculature compared with *Notch3*$^{+/+}$ (left), and the most highly differentially expressed genes in the *Pdgfb*$^{ret/ret}$ brain vasculature compared with *Pdgfb*$^{ret/+}$ control (right). Note the absence of similarities between the *Notch3*$^{-/-}$ and *Pdgfb*$^{ret/ret}$ genotypes at this level of comparison. **I**, Relative expression (log2 ratio) of known markers for the blood–brain barrier (BBB), endothelial cells, astrocytes, pericytes, VSMC, and glomerular podocytes in brain vascular fragments of the different genotypes indicated. Only markers for 2 cell types seem consistently downregulated in *Notch3*$^{-/-}$ compared with *Notch3*$^{+/+}$ (ie, below *x* axis), namely VSMC (pink) and pericytes (green). Both of these groups are further downregulated in *Pdgfb*$^{ret/ret}$ (ie, right of *y* axis; *Pdgfb*$^{ret/ret}$ data obtained from reference 3. Each dot represents a probe, and 1 gene may, therefore, be represented by several probes, as indicated for *Cald1* and *NG2*. **J**, Comparison of pericyte morphology and vessel coverage in *Notch3*$^{+/+}$, *Notch3*$^{+/-}$, and *Notch3*$^{-/-}$ retinas. **K**, Quantification of pericyte coverage of capillaries in the superior and deep capillary plexuses in the adult *Notch3*$^{+/-}$ and *Notch3*$^{-/-}$ mouse retina. **L**, Pericyte coverage (CD13, in white) and endothelial cells (CD31; in red) of the brain cerebral vasculature. **M**, Quantification of capillary densities in the adult retina (μm/μm^2). **K** and **M**, n=3 per genotype. Data are presented as mean±SD. Scale bars: **A**–**C**, 50 μm; **D**–**F**, 20 μm; **J**, 20 μm; **L**, 200 μm.

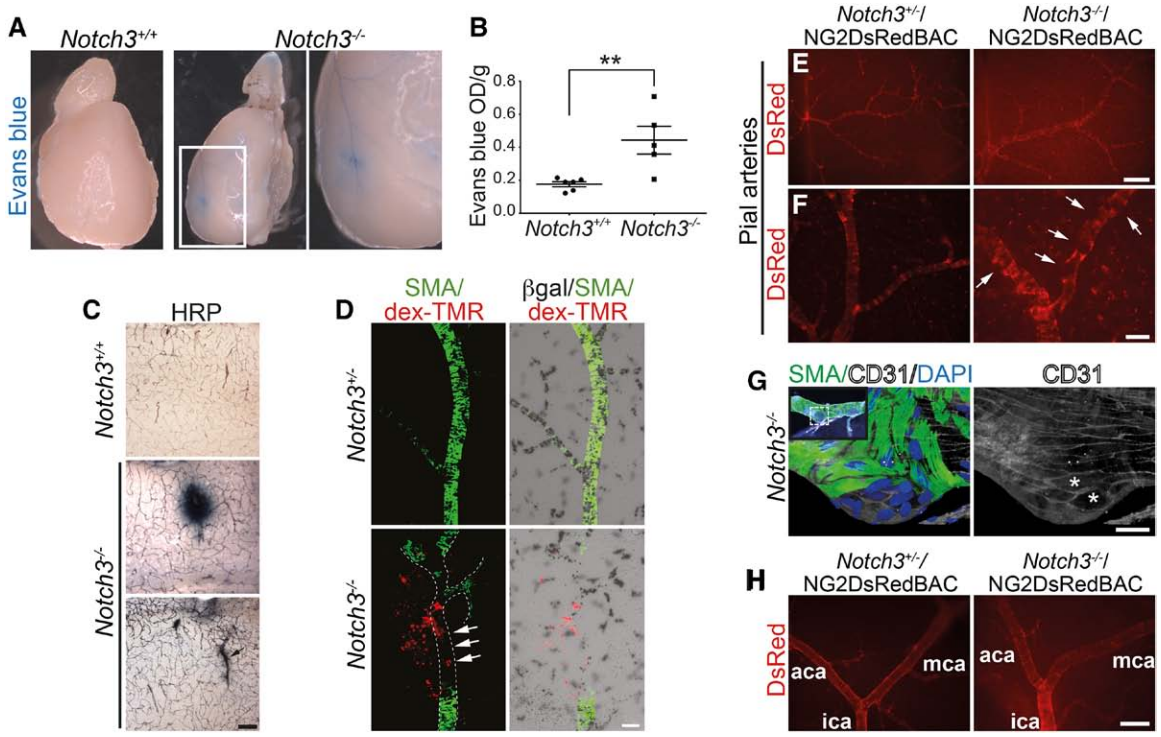


Figure 5. Loss of Notch3 results in impaired blood–brain barrier integrity. **A**, Photographs of brains from *Notch3*$^{+/+}$ and *Notch3*$^{-/-}$ mice after 16-hour Evans blue circulation. **Right**, Higher magnification view of the boxed region for *Notch3*$^{-/-}$. **B**, Quantification of Evans blue extravasation in *Notch3*$^{+/+}$ and *Notch3*$^{-/-}$ mice. *Y* axis shows optical density (OD) at 620 nm per gram of tissue in the cerebrum after 16 hours of circulation. Data are presented as mean±SEM. Total spots of leakage observed varied from 1 to 4 per brain. **C**, Extravasation of horseradish peroxidase (HRP) in the cerebral cortex of adult *Notch3*$^{-/-}$ mice after 10 minutes of circulation. **D**, Three-dimensional reconstructions of confocal image z-stacks of an adult retina primary arteriole in *Notch3*$^{+/-}$ and *Notch3*$^{-/-}$ mice after injection of 70 kDa dextran-tetramethyl rhodamine (TMR) tracer. Vascular smooth cells (VSMC) are visualized by α-smooth muscle actin (SMA) immunostaining (in green) and β-galactosidase (β-gal; X-gal staining, in black). Arrows denote leakage of tracer (in red) from an area devoid of VSMC coverage. Dotted line indicates the contour of the vessel. The tracer was circulating for 16 hours. **E** and **F**, Dorsal view of the brains of *Notch3*$^{+/-}$ and *Notch3*$^{-/-}$ mice expressing DsRed in mural cells (NG2DsRedBAC). Dilated vessels are seen in the *Notch3*$^{-/-}$ vasculature and arrows point to aneurysms in pial arteries of a *Notch3*$^{-/-}$ mouse brain. **G**, High magnification view of an aneurysm in a *Notch3*$^{-/-}$ brain pial artery immunostained with antibodies to SMA, CD31, and counterstained with 4',6-diamidino-2-phenylindole. Asterisks show distorted shape of endothelial cells. **H**, Representative segment of the Circle of Willis in *Notch3*$^{+/-}$ and *Notch3*$^{-/-}$ mice on an NG2DsRedBAC background (aca indicates anterior cerebral artery; ica, internal carotid artery; and mca, middle cerebral artery). **B**, n=5 to 6 per genotype. Scale bars: **C**, 20 μm; **D**, 40 μm; **E**, 400 μm; **F**, 100 μm; **G**, 30 μm; **H**, 400 μm. **P=0.008.

however, seemed rare in relation to the consistent loss of arterial VSMC. The sporadic nature of loss of vessel integrity was even more clearly demonstrated when looking at the retina. We analyzed retinas of adult *Notch3*$^{-/-}$ animals after injection of horseradish peroxidase or tetramethyl rhodamine-dextran (70 kDa) and leakage of tracer was observed in only 1 of 12 retinas analyzed, despite extensive loss of VSMC coverage in all retinas (Figure 5D). This shows that VSMC loss per se does not induce altered vessel permeability but rather leads to local vessel damage, causing intermittent leakage. To further address this issue, we crossed the *Notch3*$^{-/-}$ mice with NG2DsRedBAC reporter mice which express the fluorescent reporter DsRed from NG2 regulatory elements.[28] In *Notch3*$^{-/-}$/NG2-DsRedBAC mice, we found that pial arteries were dilated (Figure 5E) and that local gaps in VSMC coverage (Figure 5F) correlated with the appearance of aneurysms (Figure 5G). Interestingly, the Circle of Willis did not exhibit any apparent VSMC gaps but was nevertheless dilated (Figure 5H). In summary, these studies reveal a vessel integrity problem in *Notch3*$^{-/-}$ mice, leading to arterial dilation and aneurysm formation.

Notch3-Deficiency Leads to Fibrin Deposition in the Retinal Vasculature

Reduced vessel integrity can also be indicated by extravasation of endogenous plasma proteins. Insoluble fibrin is the end-product of thrombin cleavage of soluble fibrinogen circulating in the blood, and fibrin accumulation on a vessel wall is an indicator of vascular damage. Accumulation of extravascular fibrin in the brain has been shown to accelerate neurovascular damage.[29] Immunostaining for plasma-derived fibrinogen (340 kDa) revealed sporadic fibrinogen/fibrin deposits associated with retinal arterioles in *Notch3*$^{-/-}$ mice but not in controls (Figure 6A′). Both extra- and intravascular fibrin was observed and correlated spatially with defective VSMC coverage (Figure 6A″). Three-dimensional analysis of confocal images shows fibrin inside the vessel wall (Figure 6B; Figure IX in the online-only Data Supplement) suggesting regional penetration of fibrinogen through the endothelial layer and fibrin deposition within the medial layer. Like the extravasation of exogenous tracers, these regions appeared sporadic and were not associated with every VSMC gap. Occasionally, fibrin was also observed in retinal capillaries as intense

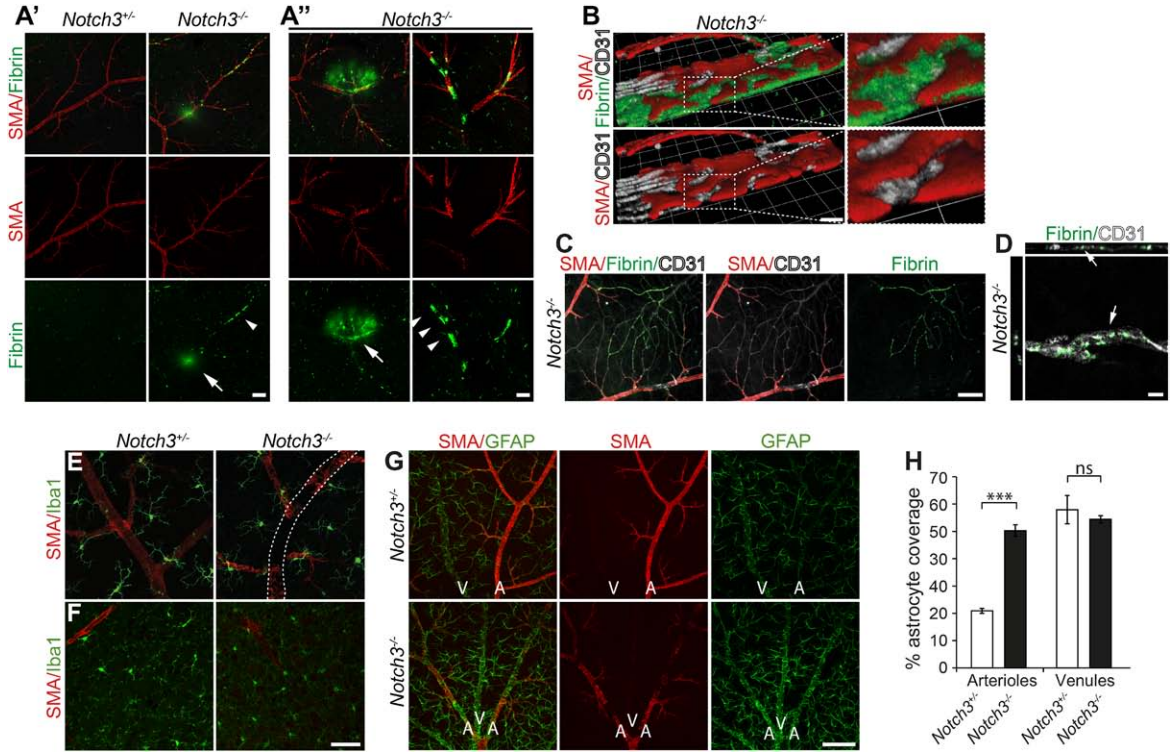


Figure 6. Fibrin deposition and enhanced astrocyte coverage of arterioles in the *Notch3*$^{-/-}$ retinal vasculature. **A′–A″**, Immunostaining with fibrinogen and α-smooth muscle actin (SMA) antibodies in adult *Notch3*$^{+/-}$ and *Notch3*$^{-/-}$ retinas showing fibrin leakage from (arrows), and accumulation within (arrowheads) primary radial arterioles. **B**, Three-dimensional opacity image of a section of an adult *Notch3*$^{-/-}$ primary retinal arteriole immunostained for fibrinogen, CD31 and SMA. **Right**, High magnification view of the boxed area. **C**, The capillary bed of an adult *Notch3*$^{-/-}$ retina immunostained for fibrinogen, CD31, and SMA. **D**, Xyz-view confocal image of an adult *Notch3*$^{-/-}$ retinal capillary immunostained for fibrin and CD31. Arrows highlight regions where fibrin is clearly found contained within the vessel lumen surrounded by the endothelial cell layer (CD31; white). **E** and **F**, Confocal images of tissue immunostained for Iba1 to visualize microglia in the retina (**E**) and brain (**F**) of *Notch3*$^{+/-}$ and *Notch3*$^{-/-}$ mice. **G**, Immunostaining with antibodies to glial fibrillary acidic protein (GFAP) shows accumulation of astrocytes around arterioles in *Notch3*$^{-/-}$ mice. **H**, Quantification of percentage coverage of arterioles and venules in adult *Notch3*$^{+/-}$ and *Notch3*$^{-/-}$ mouse retinas. **A′–A″**, Fibrin leakage into parenchyma (n=1/8 +/– and 4/9 –/–); fibrin surrounding arterioles (n=1/8 +/– and 9/9$^{-/-}$); and **C**, fibrin within capillaries (n=1/5 +/– and 5/9 $^{-/-}$). Data are presented as mean±SD. **H**, n=3 mice per genotype. Scale bars: **A′**, 100 μm; **A″**, 50 μm; **B**, 8.72 μm/unit; **C**, 100 μm; **D**, 5 μm; **E–F**, 50 μm; **G**, 200 μm. ***P*=0.008; ****P*<0.005.

punctate staining revealed by confocal microscopy (Figure 6C and 6D). The cause of capillary fibrin deposition is not known, but it is possible that it reflects embolism of fibrin deposits formed upstream. We did not detect fibrin deposits in brain arteries or capillaries, even in ≤18-month-old mice (data not shown). Why there is a difference between retina and brain in this regard is unclear but may reflect the larger and more conspicuous VSMC gaps seen in the retina compared with the brain.

We next explored whether endothelial junctions were altered in the *Notch3*$^{-/-}$ mice. Immunostaining for the tight junctional proteins occludin, claudin-5, and ZO-1 in brain pial arteries revealed no obvious alteration in abundance or distribution of endothelial tight junctions, and additionally, no obvious alteration in endothelial junctions could be observed within the retina by TEM (Figure X in the online-only Data Supplement). This shows that there is no general junction breakdown, but we cannot exclude that it happens in the rare events when there is leakage.

To determine whether the observed vascular leakage leads to reactivity in the parenchyma, we analyzed the morphology and distribution of microglia and astrocytes, which both contribute to the function and repair of the neurovascular unit. Microglial morphology was indistinguishable in the different genotypes and consistent with a nonreactive state (Figure 6E and 6F). Astrocyte morphology and level of GFAP (glial fibrillary acidic protein) expression were also comparable between *Notch3*$^{-/-}$ mice and controls with the exception of an increase in GFAP-positive astrocyte coverage of the sparsely mural cell-covered primary radial arterioles in the *Notch3*$^{-/-}$ mouse retina (Figure 6G and 6H; Figure XI in the online-only Data Supplement). Collectively, these data suggest that VSMC play an important role in maintaining the integrity of vessels and that the reduced vessel integrity in the *Notch3*$^{-/-}$ mice is manifested by fibrin deposition and local reaction of astrocytes in areas devoid of VSMC.

Discussion

In this report, we have identified a novel role for Notch3 and VSMC in vascular integrity. *Notch3*$^{-/-}$ mice exhibited localized leakage of injected tracers across the BBB accompanied by weakening and bulging of the endothelium. Furthermore, there was fibrin deposition in the retinal vasculature. In arterioles, fibrin was deposited along the abluminal side of the endothelium and intermingled with VSMC, while in capillaries there was intraluminal fibrin accumulation.

Primary and Secondary Phenotypes

Our data indicate that the impairment of vascular integrity is a consequence of a primary VSMC phenotype, with morphological changes and cell degeneration only visible in arterial VSMC in the *Notch3*$^{-/-}$ brain and retina, while venous VSMC and pericytes remained normal in number and morphology. *Notch3* is also expressed in pericytes, and while it has recently been shown that Notch signaling may protect cultured retinal pericytes from light-induced cell death,[30] our data provide no evidence for a pericyte phenotype at the level of cell number, morphology and function in ≤8-month-old mice.

The progressive postnatal loss of arterial VSMC in *Notch3*$^{-/-}$ mice leads to the formation of apparent gaps in the VSMC coat, which confirms and extends previously reported results.[5–7] Interestingly, VSMC loss was not uniform along CNS arteries: gaps were more prevalent in the larger diameter arterioles closer to the origin of the optic nerve, and less frequent in the peripheral arterioles, and a similar proximo-distal distribution of VSMC defects was also observed in the brain. The loss of arterial VSMC is likely the primary morphogenetic change, leading to secondary effects on endothelial function and vascular integrity. This view is supported by our transcriptome data, which reveal changes in gene expression also in endothelial cells, although these cells do not express Notch3. Notch signaling has been implicated in the communication between endothelium and VSMC,[31] but although disruption of Jagged-1 in endothelial cells affects VSMC,[32] endothelial changes caused by a primary VSMC defect have to our knowledge not previously been demonstrated.

Progressive Loss of VSMC in *Notch3*$^{-/-}$ Mice

We provide several lines of evidence indicating that VSMC are progressively lost in *Notch3*$^{-/-}$ mice, culminating in cell death linked with an elevated level of apoptosis. First, arterial VSMC show a gradual decrease in the amount of SMA, desmin, and NG2 immunoreactivity over time. A protracted degenerative process is also supported by our TEM data. Whereas in control mice, the retinal arteriolar VSMC exist as a single layer of cells surrounded on both sides by a vascular basement membrane, *Notch3*$^{-/-}$ mice display a range of VSMC morphologies, spanning from normal to altered ultrastructural features of living cells, and extending to various stages of cell disintegration close to the gaps. All of these features were observed within the vascular basement membrane, which appeared thicker in the *Notch3*$^{-/-}$ mice and contained material with fibrillar morphology (Figure 5F, bottom), possibly arising from the fibrin leakage and perivascular deposition observed by light microscopy. The protracted decay of VSMC marker expression and altered morphology of VSMC in the vicinity of the gaps could suggest that the cell degeneration is preceded by a change in the VSMC phenotype.

To what extent this reflects the known plasticity of VSMC, for example switching between contractile and synthetic phenotypes in injury situations,[1,33] is unclear. It has previously been proposed that arterial VSMC differentiation is defective in *Notch3*$^{-/-}$ mice and that these cells may instead have acquired venous characteristics,[5] suggesting a problem with cell lineage specification or differentiation. In search of evidence for consistent changes in arterial and venous VSMC markers, we assessed arterial and venous SMC markers identified in a previous global gene expression profiling study[34] in our data set. Whereas some selected arterial VSMC markers were significantly downregulated in *Notch3*$^{-/-}$ vessels (Figure 4C), this comparison did not reveal any consistent changes in arterial or venous VSMC markers analyzed at a global level (Figure XII in the online-only Data Supplement). We observed an increase in apoptosis, as judged by caspase 3-positive staining in the *Notch3*$^{-/-}$ retina. Caspase 3-positivity was noted in the gaps, indicating that VSMC succumb by apoptosis and do not transdifferentiate to alternative fates. An increase in apoptosis is in keeping with one previous report[7] but contrasting another.[5] Interestingly, apoptosis was not evenly distributed in the vasculature but frequently observed in VSMC located precisely at the branch points along the primary radial arteriole. This was noted in all genotypes, however was increased in *Notch3*$^{-/-}$ mice. This phenomenon may be because of altered flow dynamics and stress at the branch points as it is also noted that the branch points are often sites for development of atherosclerosis.[35] Further, our ultrastructural analysis revealed a novel phenotype, where endoplasmatic reticulum morphology was altered in an otherwise morphologically normal VSMC. This phenotype was widespread in the *Notch3*$^{-/-}$ vasculature and may indicate an early step in the VSMC degeneration process, further supporting the notion that cells are lost rather than transdifferentiating. In conclusion, our gene expression data are consistent with a selective partial reduction in the number of arterial VSMC through cell death, as also demonstrated morphologically, but does not support a change in arteriovenous specification of the VSMC.

Role for Arterial VSMC in Maintaining Vascular Wall Integrity

Our data also shed light on the different roles of pericytes and arterial VSMC on vascular integrity and function in the CNS. Mural cells are critical for a functional vasculature as pericytes recently have been shown to play a key role in the development and maintenance of the BBB[3,4]; however, less is known about VSMC in this regard. As the effects of Notch3 deficiency seem to be confined to arterial VSMC, our study provides evidence that VSMC also play a role in maintaining vascular integrity in mammals. The difference in the vascular phenotype caused by pericyte and arterial VSMC loss, respectively, is however noteworthy: in pericyte-deficient *Pdgfb*$^{ret/ret}$ mice, BBB impairment was uniform within and between individuals.[3,4] In contrast, in *Notch3*$^{-/-}$ mice, BBB leakage was focal, less frequent, and did not show prevalence for specific CNS regions. In *Pdgfb*$^{ret/ret}$ mice, BBB permeability was increased via enhanced endothelial transendocytosis.[3,4] Whether this is the case also in *Notch3*$^{-/-}$ mice remains to be established. However, the local leakage of tracer dyes, presence of frequent aneurysms, and the accumulation of debris in the vessel wall all suggest local rupturing of the

arterial wall as a possible mechanism of BBB impairment in *Notch3*$^{-/-}$ mice. Although endothelial cell junctions appeared structurally normal by immunostaining and TEM (Figure X in the online-only Data Supplement), we cannot exclude a local breakdown of endothelial junctions at the site of the focal leakage. A role for Notch3 in vascular integrity is corroborated by 2 recent studies in zebrafish, where *Notch3* mutations caused bulging blood vessels and hemorrhage.[36,37] Although this underscores the importance of Notch3 for vasculature in both zebrafish and mammals, the underlying mechanisms may be distinct. In zebrafish, it seems that the breakdown of vascular integrity is mediated by an effect of *Notch3* deficiency in pericytes,[36,37] whereas our data demonstrate that pericytes are not involved in the vascular integrity problems observed in *Notch3*$^{-/-}$ mice. The fact that the Notch downstream gene *Hey1* is differentially affected in Notch3 mutant zebrafish and *Notch3*$^{-/-}$ mice[5,37] further supports distinct mechanisms.

Possible Implications for CADASIL Pathogenesis

The proposed role for Notch3 in maintaining arterial integrity by securing long-term functionality and survival of VSMC of certain caliber CNS arteries/arterioles is interesting in relation to the role of Notch deregulation in CADASIL. Although the link between NOTCH3 mutations and CADASIL is well established, it is not yet known to what extent CADASIL-mutated NOTCH3 results in neomorphic functions or whether some of the disease aspects can be attributed to a loss of function of NOTCH3 activity. It is clear that *Notch3*$^{-/-}$ mice do not recapitulate the disease pathology with regard to GOM formation and white matter degeneration, arguing against a strict loss-of-function modality. Two presumed loss-of-function NOTCH3 mutations did not associate with typical CADASIL-like pathologies, but both occurred in heterozygote individuals, hence being analogous to *Notch3*$^{+/-}$ mice which lack an overt VSMC phenotype.[38,39] At present, it remains debatable whether reduced Notch signaling also contributes to the disease. Some CADASIL-mutated NOTCH3 receptors show reduced signaling,[18,19,40] and patients with CADASIL have fragile vasculature, such that angiographic analysis is avoided.[41] This is in line with the link between loss of Notch3 activity and the aneurysm-like changes and focal BBB leakage observed in this study. Similarly, the accumulation of fibrin observed here is of interest as vascular fibrin accumulation is well documented in patients with CADASIL[42,43] and could be a common downstream consequence of both degeneration or deregulation of VSMC.

In conclusion, we show that arterial VSMC are important for maintenance of vascular integrity in the CNS and define Notch3 as a key gene in this process. These data are of interest to better understand how various types of mural cells contribute to a functional vascular system.

Acknowledgments

We are grateful to Susanne Bergstedt, Pia Peterson, Jana Chmielniakova, Cecilia Olsson, Yvonne Josefsson, and Helene Leksell for their skilled technical assistance.

Sources of Funding

This study was supported by grants from the European Research Council (AdG BBBARRIER; NotchIT), the Leducq Foundation, the Swedish Cancer Society and Swedish Research Council, Knut och Alice Wallenbergs Stiftelse, Inga-Britt och Arne Lundbergs Stiftelse and Torsten och Ragnar Söderbergs Stiftelse, Karolinska Institutet, and Uppsala University. T.L. Henshall holds a postdoctoral fellowship from Svenska Sällskapet för Medicinsk Forskning.

Disclosures

None.

References

1. Alexander MR, Owens GK. Epigenetic control of smooth muscle cell differentiation and phenotypic switching in vascular development and disease. *Annu Rev Physiol*. 2012;74:13–40. doi: 10.1146/annurev-physiol-012110-142315.
2. Armulik A, Genové G, Betsholtz C. Pericytes: developmental, physiological, and pathological perspectives, problems, and promises. *Dev Cell*. 2011;21:193–215. doi: 10.1016/j.devcel.2011.07.001.
3. Armulik A, Genové G, Mäe M, Nisancioglu MH, Wallgard E, Niaudet C, He L, Norlin J, Lindblom P, Strittmatter K, Johansson BR, Betsholtz C. Pericytes regulate the blood-brain barrier. *Nature*. 2010;468:557–561. doi: 10.1038/nature09522.
4. Daneman R, Zhou L, Kebede AA, Barres BA. Pericytes are required for blood-brain barrier integrity during embryogenesis. *Nature*. 2010;468:562–566. doi: 10.1038/nature09513.
5. Domenga V, Fardoux P, Lacombe P, Monet M, Maciazek J, Krebs LT, Klonjkowski B, Berrou E, Mericskay M, Li Z, Tournier-Lasserve E, Gridley T, Joutel A. Notch3 is required for arterial identity and maturation of vascular smooth muscle cells. *Genes Dev*. 2004;18:2730–2735. doi: 10.1101/gad.308904.
6. Jin S, Hansson EM, Tikka S, Lanner F, Sahlgren C, Farnebo F, Baumann M, Kalimo H, Lendahl U. Notch signaling regulates platelet-derived growth factor receptor-beta expression in vascular smooth muscle cells. *Circ Res*. 2008;102:1483–1491. doi: 10.1161/CIRCRESAHA.107.167965.
7. Liu H, Zhang W, Kennard S, Caldwell RB, Lilly B. Notch3 is critical for proper angiogenesis and mural cell investment. *Circ Res*. 2010;107:860–870. doi: 10.1161/CIRCRESAHA.110.218271.
8. Andersson ER, Sandberg R, Lendahl U. Notch signaling: simplicity in design, versatility in function. *Development*. 2011;138:3593–3612. doi: 10.1242/dev.063610.
9. Hellström M, Phng LK, Hofmann JJ, et al. Dll4 signalling through Notch1 regulates formation of tip cells during angiogenesis. *Nature*. 2007;445:776–780. doi: 10.1038/nature05571.
10. Gridley T. Notch signaling in the vasculature. *Curr Top Dev Biol*. 2010;92:277–309. doi: 10.1016/S0070-2153(10)92009-7.
11. Lardelli M, Dahlstrand J, Lendahl U. The novel Notch homologue mouse Notch 3 lacks specific epidermal growth factor-repeats and is expressed in proliferating neuroepithelium. *Mech Dev*. 1994;46:123–136.
12. Larsson C, Lardelli M, White I, Lendahl U. The human NOTCH1, 2, and 3 genes are located at chromosome positions 9q34, 1p13-p11, and 19p13.2-p13.1 in regions of neoplasia-associated translocation. *Genomics*. 1994;24:253–258. doi: 10.1006/geno.1994.1613.
13. Li X, Zhang X, Leathers R, Makino A, Huang C, Parsa P, Macias J, Yuan JX, Jamieson SW, Thistlethwaite PA. Notch3 signaling promotes the development of pulmonary arterial hypertension. *Nat Med*. 2009;15:1289–1297. doi: 10.1038/nm.2021.
14. Joutel A, Corpechot C, Ducros A, et al. Notch3 mutations in CADASIL, a hereditary adult-onset condition causing stroke and dementia. *Nature*. 1996;383:707–710. doi: 10.1038/383707a0.
15. Lee JH, Bacskai BJ, Ayata C. Genetic animal models of cerebral vasculopathies. *Prog Mol Biol Transl Sci*. 2012;105:25–55. doi: 10.1016/B978-0-12-394596-9.00002-0.
16. Baudrimont M, Dubas F, Joutel A, Tournier-Lasserve E, Bousser MG. Autosomal dominant leukoencephalopathy and subcortical ischemic stroke. A clinicopathological study. *Stroke*. 1993;24:122–125.
17. Joutel A. Pathogenesis of CADASIL: transgenic and knock-out mice to probe function and dysfunction of the mutated gene, Notch3, in the cerebrovasculature. *Bioessays*. 2011;33:73–80. doi: 10.1002/bies.201000093.

18. Karlström H, Beatus P, Dannaeus K, Chapman G, Lendahl U, Lundkvist J. A CADASIL-mutated Notch 3 receptor exhibits impaired intracellular trafficking and maturation but normal ligand-induced signaling. *Proc Natl Acad Sci U S A*. 2002;99:17119–17124. doi: 10.1073/pnas.252624099.
19. Arboleda-Velasquez JF, Manent J, Lee JH, et al. Hypomorphic Notch 3 alleles link Notch signaling to ischemic cerebral small-vessel disease. *Proc Natl Acad Sci U S A*. 2011;108:E128–E135. doi: 10.1073/pnas.1101964108.
20. Joutel A, Monet-Leprêtre M, Gosele C, Baron-Menguy C, Hammes A, Schmidt S, Lemaire-Carrette B, Domenga V, Schedl A, Lacombe P, Hubner N. Cerebrovascular dysfunction and microcirculation rarefaction precede white matter lesions in a mouse genetic model of cerebral ischemic small vessel disease. *J Clin Invest*. 2010;120:433–445. doi: 10.1172/JCI39733.
21. Monet-Leprêtre M, Haddad I, Baron-Menguy C, Fouillot-Panchal M, Riani M, Domenga-Denier V, Dussaule C, Cognat E, Vinh J, Joutel A. Abnormal recruitment of extracellular matrix proteins by excess Notch3 ECD: a new pathomechanism in CADASIL. *Brain*. 2013;136(pt 6):1830–1845. doi: 10.1093/brain/awt092.
22. Belin de Chantemèle EJ, Retailleau K, Pinaud F, Vessières E, Bocquet A, Guihot AL, Lemaire B, Domenga V, Baufreton C, Loufrani L, Joutel A, Henrion D. Notch3 is a major regulator of vascular tone in cerebral and tail resistance arteries. *Arterioscler Thromb Vasc Biol*. 2008;28:2216–24.
23. Arboleda-Velasquez JF, Zhou Z, Shin HK, Louvi A, Kim HH, Savitz SI, Liao JK, Salomone S, Ayata C, Moskowitz MA, Artavanis-Tsakonas S. Linking Notch signaling to ischemic stroke. *Proc Natl Acad Sci U S A*. 2008;105:4856–4861. doi: 10.1073/pnas.0709867105.
24. Mitchell KJ, Pinson KI, Kelly OG, et al. Functional analysis of secreted and transmembrane proteins critical to mouse development. *Nat Genet*. 2001;28:241–249. doi: 10.1038/90074.
25. Leimeister C, Schumacher N, Steidl C, Gessler M. Analysis of HeyL expression in wild-type and Notch pathway mutant mouse embryos. *Mech Dev*. 2000;98:175–178.
26. Zhao N, Liu H, Lilly B. Reciprocal regulation of syndecan-2 and Notch signaling in vascular smooth muscle cells. *J Biol Chem*. 2012;287:16111–16120. doi: 10.1074/jbc.M111.322107.
27. Daneman R, Zhou L, Agalliu D, Cahoy JD, Kaushal A, Barres BA. The mouse blood-brain barrier transcriptome: a new resource for understanding the development and function of brain endothelial cells. *PLoS One*. 2010;5:e13741. doi: 10.1371/journal.pone.0013741.
28. Zhu X, Bergles DE, Nishiyama A. NG2 cells generate both oligodendrocytes and gray matter astrocytes. *Development*. 2008;135:145–157. doi: 10.1242/dev.004895.
29. Paul J, Strickland S, Melchor JP. Fibrin deposition accelerates neurovascular damage and neuroinflammation in mouse models of Alzheimer's disease. *J Exp Med*. 2007;204:1999–2008. doi: 10.1084/jem.20070304.
30. Arboleda-Velasquez JF, Primo V, Graham M, James A, Manent J, D'Amore PA. Notch signaling functions in retinal pericyte survival. *Invest Ophthalmol Vis Sci*. 2014;55:5191–5199. doi: 10.1167/iovs.14-14046.
31. Liu H, Kennard S, Lilly B. NOTCH3 expression is induced in mural cells through an autoregulatory loop that requires endothelial-expressed JAGGED1. *Circ Res*. 2009;104:466–475. doi: 10.1161/CIRCRESAHA.108.184846.
32. High FA, Lu MM, Pear WS, Loomes KM, Kaestner KH, Epstein JA. Endothelial expression of the Notch ligand Jagged1 is required for vascular smooth muscle development. *Proc Natl Acad Sci U S A*. 2008;105:1955–1959. doi: 10.1073/pnas.0709663105.
33. Nguyen AT, Gomez D, Bell RD, et al. Smooth muscle cell plasticity: fact or fiction? *Circ Res*. 2013;112:17–22. doi: 10.1161/CIRCRESAHA.112.281048.
34. Chi JT, Rodriguez EH, Wang Z, Nuyten DS, Mukherjee S, van de Rijn M, van de Vijver MJ, Hastie T, Brown PO. Gene expression programs of human smooth muscle cells: tissue-specific differentiation and prognostic significance in breast cancers. *PLoS Genet*. 2007;3:1770–1784. doi: 10.1371/journal.pgen.0030164.
35. Chiu JJ, Chien S. Effects of disturbed flow on vascular endothelium: pathophysiological basis and clinical perspectives. *Physiol Rev*. 2011;91:327–387. doi: 10.1152/physrev.00047.2009.
36. Zaucker A, Mercurio S, Sternheim N, Talbot WS, Marlow FL. Notch3 is essential for oligodendrocyte development and vascular integrity in zebrafish. *Dis Model Mech*. 2013;6:1246–1259. doi: 10.1242/dmm.012005.
37. Wang Y, Pan L, Moens CB, Appel B. Notch3 establishes brain vascular integrity by regulating pericyte number. *Development*. 2014;141:307–317. doi: 10.1242/dev.096107.
38. Rutten JW, Boon EM, Liem MK, Dauwerse JG, Pont MJ, Vollebregt E, Maat-Kievit AJ, Ginjaar HB, Lakeman P, van Duinen SG, Terwindt GM, Lesnik Oberstein SA. Hypomorphic NOTCH3 alleles do not cause CADASIL in humans. *Hum Mutat*. 2013;34:1486–1489. doi: 10.1002/humu.22432.
39. Joutel A. Loss-of-function mutation in the NOTCH3 gene: simply a polymorphism? *Hum Mutat*. 2013;34:v. doi: 10.1002/humu.22198.
40. Joutel A, Monet M, Domenga V, Riant F, Tournier-Lasserve E. Pathogenic mutations associated with cerebral autosomal dominant arteriopathy with subcortical infarcts and leukoencephalopathy differently affect Jagged1 binding and Notch3 activity via the RBP/JK signaling Pathway. *Am J Hum Genet*. 2004;74:338–347. doi: 10.1086/381506.
41. Dichgans M, Joutel A, Chabriat H. Letter by Dichgans et al regarding article, "Peripheral artery disease as a manifestation of cerebral autosomal dominant arteriopathy with subcortical infarcts and leukoencephalopathy (CADASIL) and practical implications". *Circulation*. 2013;128:e363. doi: 10.1161/CIRCULATIONAHA.113.003657.
42. Ratzinger G, Ransmayr G, Romani N, Zelger B. CADASIL-an unusual manifestation with prominent cutaneous involvement. *Br J Dermatol*. 2005;152:346–349. doi: 10.1111/j.1365-2133.2004.06264.x.
43. Choudhary S, Torchia D, Romanelli P. with Subcortical Infarcts and Leukoencephalopathy (CADASIL). 2013;6:29–33.

Significance

To what extent mural cells, and in particular vascular smooth muscle cells, contribute to barrier functions in larger vessels is largely unknown. In this report, we provide evidence for a role of vascular smooth muscle cells in the control of vascular integrity. We observe that in Notch3 knockout mice, vascular smooth muscle cells are progressively lost from resistance arteries in the brain and retina by degeneration, resulting in focal disruptions of the blood–brain barrier and deposition of fibrin. These data reveal a critical role for Notch3 and vascular smooth muscle cells in blood vessel integrity and blood–brain barrier function in the mammalian vasculature and are important to better understand Notch-related vascular pathogenesis.

Arteriosclerosis, Thrombosis, and Vascular Biology

JOURNAL OF THE AMERICAN HEART ASSOCIATION

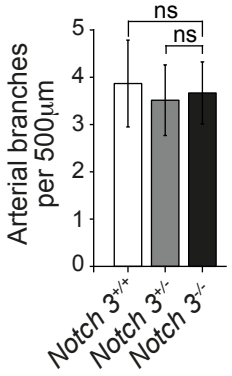
Notch3 Is Necessary for Blood Vessel Integrity in the Central Nervous System

Tanya L. Henshall, Annika Keller, Liqun He, Bengt R. Johansson, Elisabet Wallgard, Elisabeth Raschperger, Maarja Andaloussi Mäe, Shaobo Jin, Christer Betsholtz and Urban Lendahl

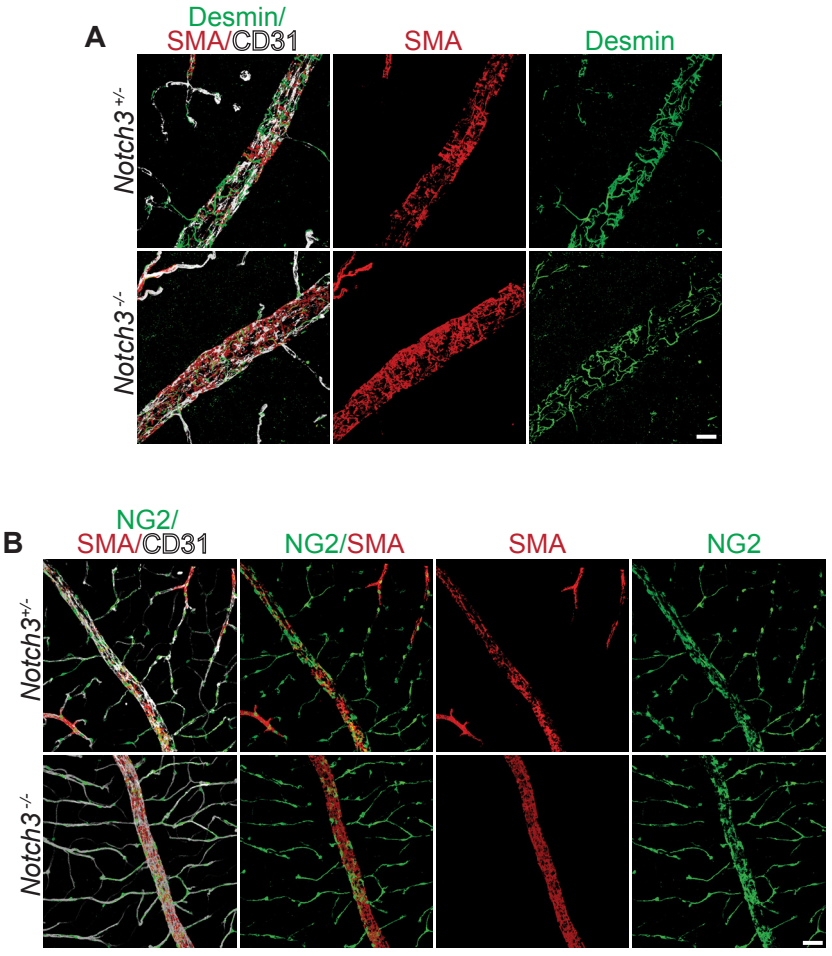
Arterioscler Thromb Vasc Biol. 2015;35:409-420; originally published online December 4, 2014;
doi: 10.1161/ATVBAHA.114.304849
Arteriosclerosis, Thrombosis, and Vascular Biology is published by the American Heart Association, 7272 Greenville Avenue, Dallas, TX 75231

Print ISSN: 1079-5642. Online ISSN: 1524-4636

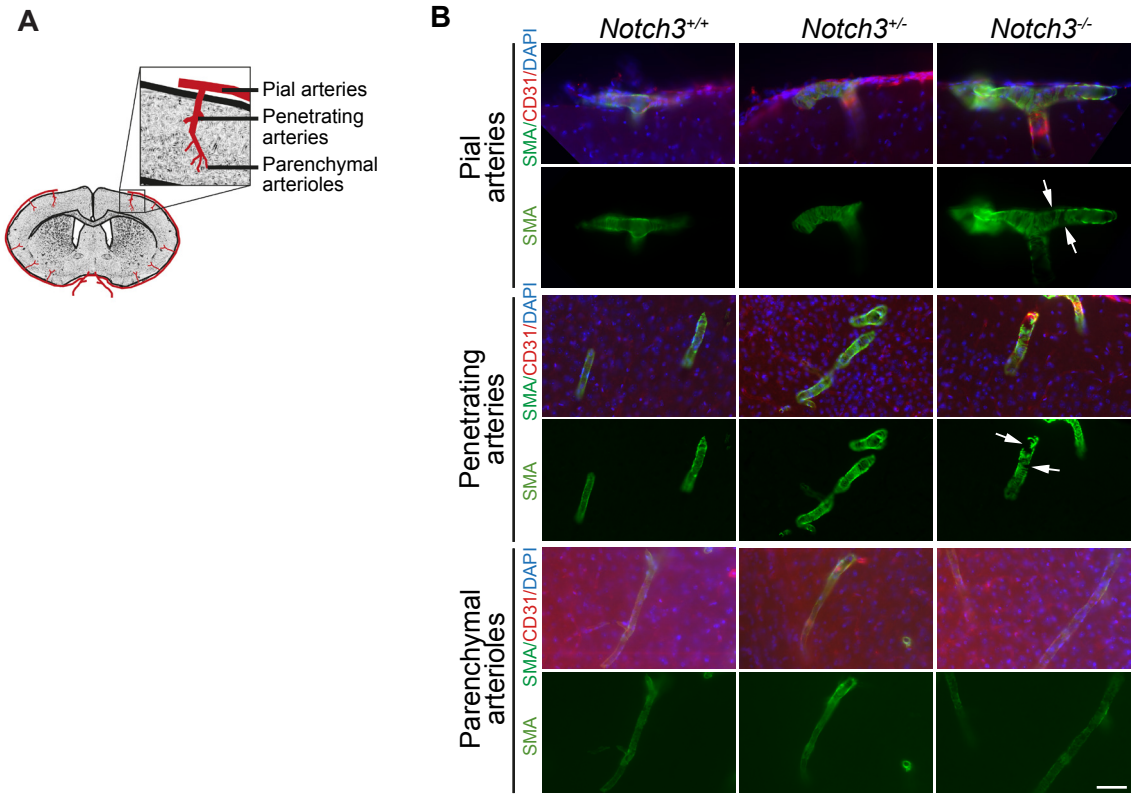
Supplemental Material



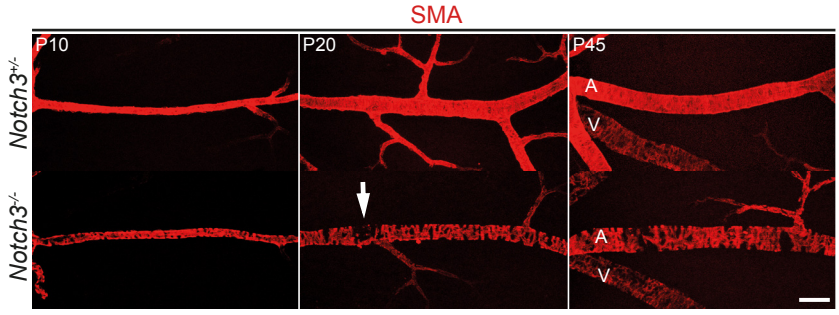
Supplemental Figure I: Vessel branching is not altered in adult *Notch3*$^{-/-}$ retinas. Quantitation of number of arterial branches in the central zone (820-1640 μm) of primary radial arterioles of adult *Notch3*$^{+/+}$, *Notch3*$^{+/-}$ and *Notch3*$^{-/-}$ mouse retinas (see Figure 1). Data are presented as mean +/- s.d. n = 4 per genotype.



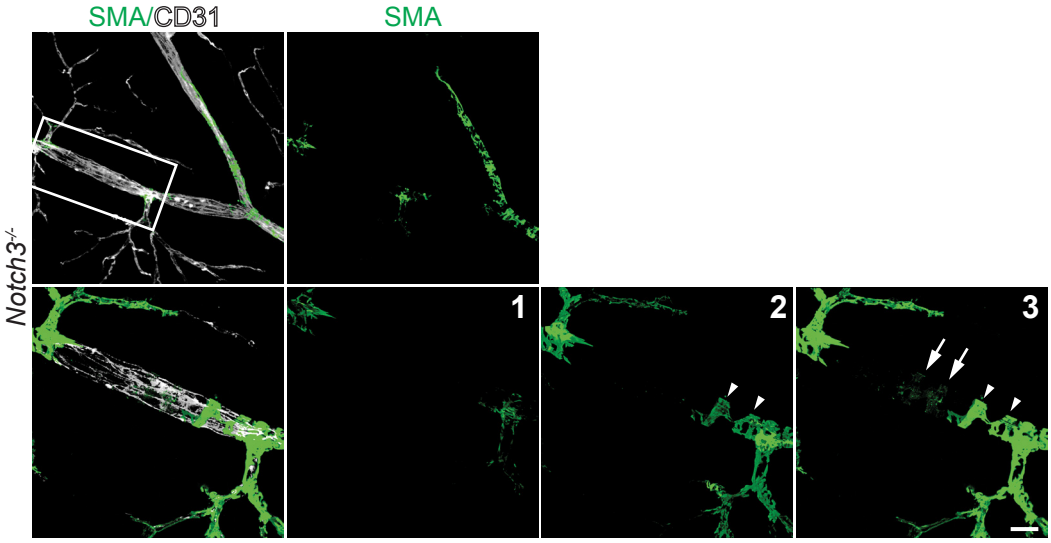
Supplemental Figure II: VSMC coverage of venules is not altered in the adult *Notch3*$^{-/-}$ retina. A and **B**, Visualization of SMA (VSMC, in red) and CD31 (endothelial cells, in white) with two other markers of VSMC, desmin (**A**) and NG2 (**B**) (in green) shows no change in VSMC coverage along the venules in *Notch3*$^{-/-}$ animals. Scale bars: **A** – 20 μm; **B** – 45 μm.



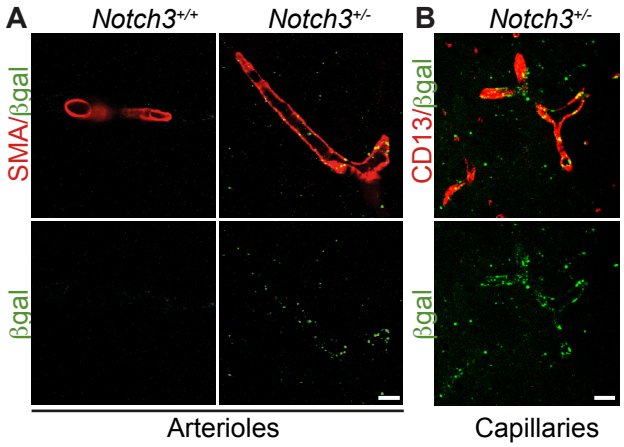
Supplemental Figure III: Gaps in SMA staining are primarily observed in larger cerebral arteries in the *Notch3*$^{-/-}$ brain. A, Schematic depiction of the hierarchy of the brain vasculature in the adult mouse in coronal section. **B**, Immunostaining of SMA (in green) and CD31 (in red) in three types of arteries in the adult brain demonstrating clear gaps (arrows) in VSMC coverage in pial and penetrating arteries. Nucleus is stained with DAPI (blue). Scale bar: **B** – 50 μm.



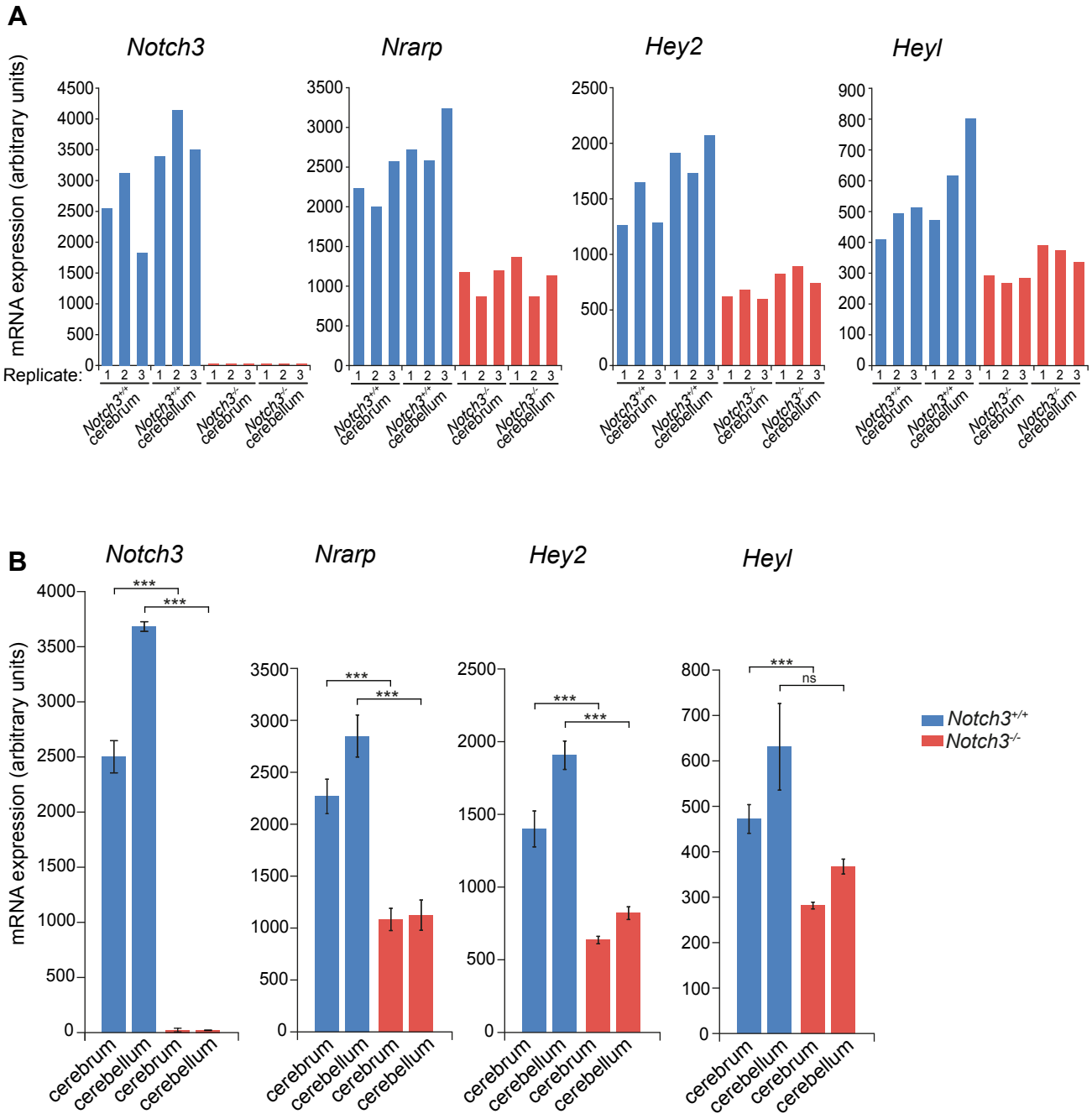
Supplemental Figure IV: Progressive loss of *Notch3*$^{-/-}$ VSMC from early in development. Confocal images showing VSMC coverage (in red) of primary radial arterioles in *Notch3*$^{+/-}$ and *Notch3*$^{-/-}$ mouse retinas during early development. The arrow demonstrates a gap in VSMC coverage from P20. Scale bar: 50 μm.



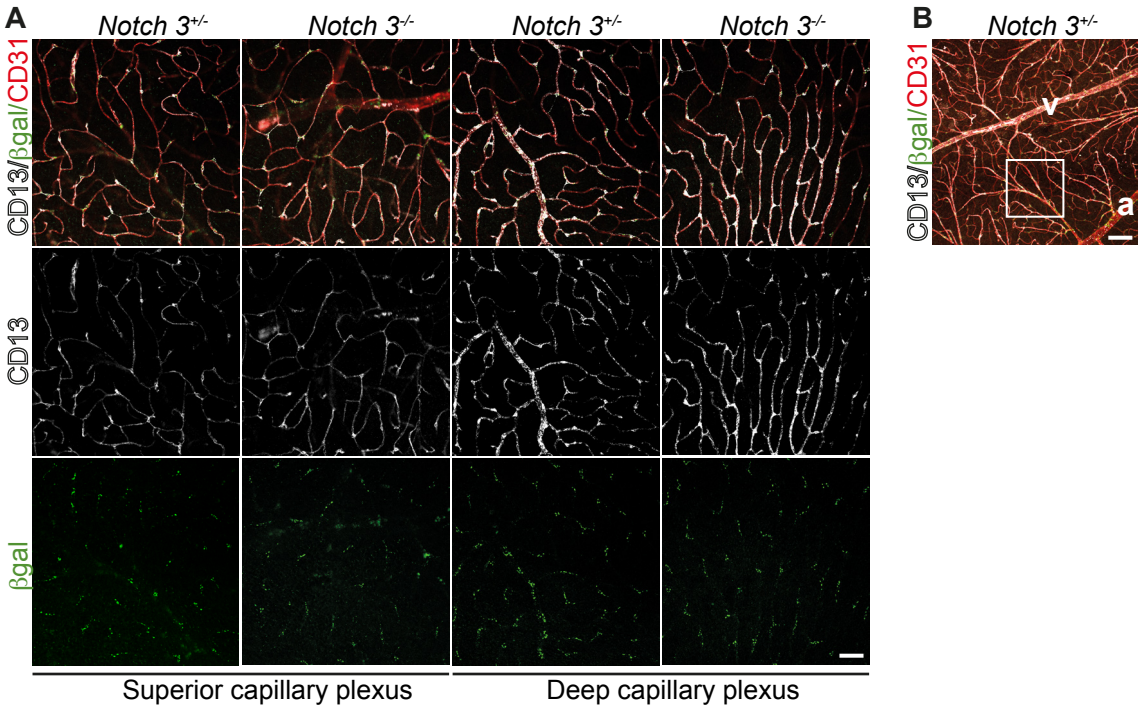
Supplemental Figure V: Weak SMA expression in VSMC revealed close to gaps in adult *Notch3*$^{-/-}$ retina. Confocal images of a retinal artery. Endothelium is visualized by CD31 immunostaining (in white), and VSMC by SMA immunostaining (in green). Lower panels show magnification of the boxed area. Increasing gain in confocal settings for the SMA staining in 1, 2 and 3 reveal VSMC with reduced SMA expression (arrowheads in 2 and arrows in 3) compared to their neighbors. Scale bar: 45 μm.



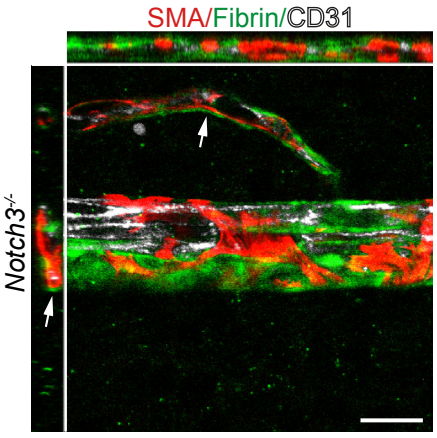
Supplemental Figure VI: Notch3 is expressed by mural cells in the brain. A and **B,** Immunostaining with antibodies against β-gal, and SMA (**A**; VSMC) or CD13 (**B**; pericytes) demonstrates colocalisation of Notch3 with VSMC and pericytes in the *Notch3*$^{+/-}$ brain. No β-gal was detected in *Notch3*$^{+/+}$ brain. Scale bars: A – 50 μm; B – 25 μm.



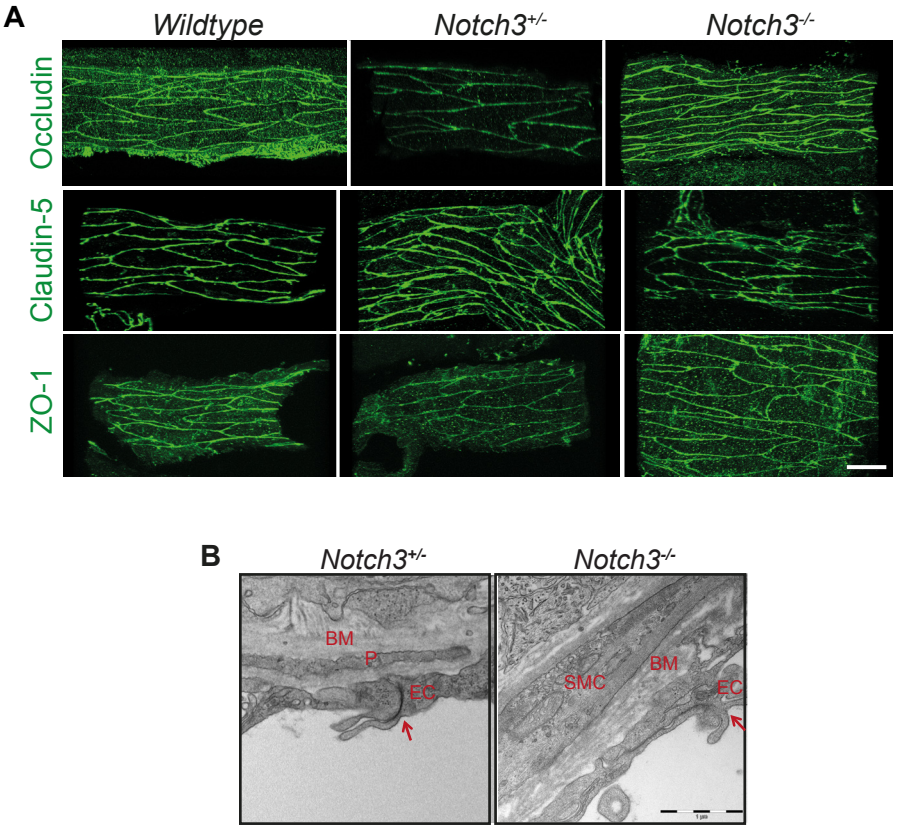
Supplemental Figure VII: Expression of *Notch3* and Notch target genes. Graphs show down-regulation of *Notch3* and Notch target genes (*Nrarp, Hey2* and *Hey-like* (*Heyl*) in all biological replicates and in both cerebrum and cerebellum (**A**) in *Notch3*$^{-/-}$ brain vasculature. Comparison of all biological replicates shows statistically significant change in expression levels (**B**). Excerpts are from Supplemental Table I. Error bars represent s.e.m. ***P< 0.005.



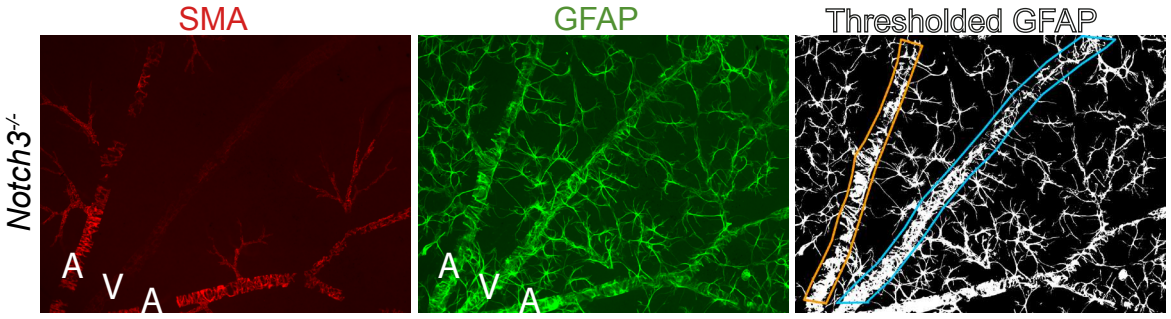
Supplemental Figure VIII: Quantitation of pericyte coverage in the adult mouse retina of *Notch3*$^{-/-}$ and control. A, B-gal, CD13 and CD31 immunoreactivity in superior and deep capillary plexuses in *Notch3*$^{+/-}$ and *Notch3*$^{-/-}$ mice. **B**, Low magnification image of a *Notch3*$^{+/-}$ mouse retina showing a region selected for quantitation of pericytes between a venule and an arteriole. The superior and deep capillary plexuses are located just posterior to the primary radial arteriole layer shown in this image (**B**). a – arteriole, v – venule. Scale bars: **A** – 50 μm; **B** – 25 μm.



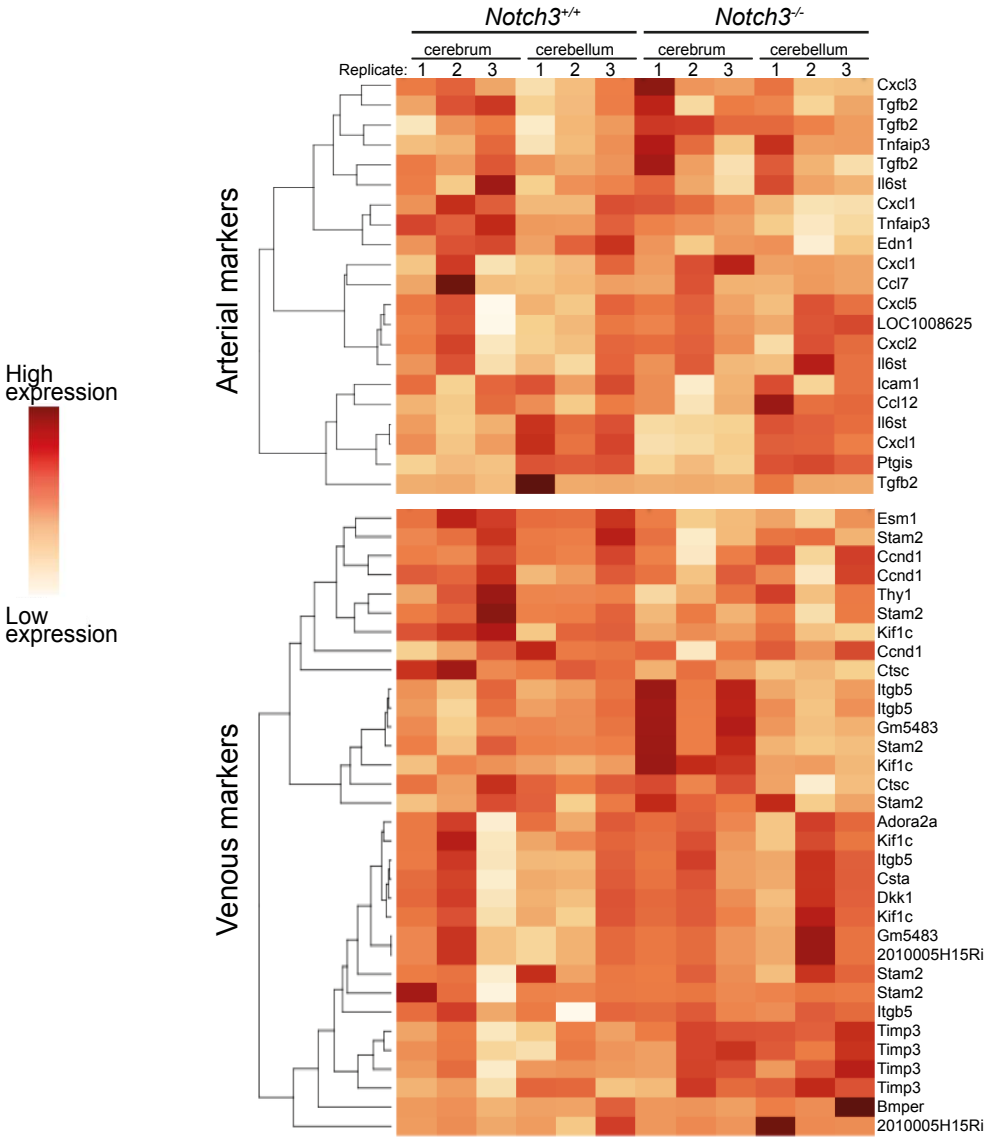
Supplemental Figure IX: Fibrin is found outside of the endothelial and VSMC layers in the *Notch3*$^{-/-}$ retina. Xyz view-confocal image of a retinal primary arteriole in a *Notch3*$^{-/-}$ animal. VSMC were visualized by SMA staining (in red), endothelium by CD31 staining (in white). Note the deposition of fibrin (in green) in the vessel wall. Scale bar: 15 μm.



Supplemental Figure X: Loss of Notch3 expression does not alter the distribution of endothelial tight junctional proteins in brain pial vessels, or ultrastructure of retinal arterioles. A, Representative confocal images showing immunostaining of brain pial arteries with antibodies against tight junctional proteins, Occludin, Claudin-5 and ZO-1 (green). **B**, TEM analysis of retinal arterioles showing a junction between endothelial cells (arrows) in a *Notch3*$^{+/-}$ control vessel and a *Notch3*$^{-/-}$ vessel, both displaying typical ultrastructural features. (SMC – smooth muscle cell; EC – endothelial cell; BM – basement membrane; P - pericyte). Scale bars: **A** – 20 μm; **B** – 1 μm.



Supplemental Figure XI: Quantitation of astrocyte coverage of vessels in the adult *Notch3*$^{-/-}$ retina. Confocal images to describe the quantitation method for determining % coverage of GFAP^{+} (green) astrocytes in the retina (See also Supplemental Methods in the online-only Data Supplement). SMA staining (in red) allows identification of arterioles (A) and venules (V). GFAP images of the same region (middle) were converted to 8-bit greyscale then autothresholded using the Li method in Image J (image shown right). Regions of interest (rois) were then drawn around arterioles (orange) and venules (blue) and % thresholded area value used to determine the % coverage of each vessel by GFAP expressing astrocytes.



Supplemental Figure XII: Heat maps of arterial and venous VSMC marker expression in *Notch3*$^{-/-}$ and wildtype brain vascular fragments. The markers displayed were identified in reference [1]. Note the absence of consistent changes (up or down) in both groups of markers in the absence of Notch3.

Supplemental Tables

Supplemental Table I: All downregulated transcripts in brain microvasculature of *Notch3*$^{-/-}$ vs wildtype (WT)

Affymetrix probe set ID	Cerebrum N3 $^{-/-}$ vs WT (log2)	Cerebellum N3$^{-/-}$ vs WT (log2)	Average fold (log2)	P value	ENTREZ ID	Symbol	Gene Name
1421965_s_at	-8.55	-8.77	-8.66	2.22E-11	18131	Notch3	notch 3
1450357_a_at	-7.17	-6.65	-6.91	1.09E-12	12458	Ccr6	chemokine (C-C motif) receptor 6
1419476_at	-6.49	-5.73	-6.11	7.89E-08	58860	Adamdec1	ADAM-like, decysin 1
1421964_at	-4.33	-5.31	-4.82	2.05E-07	18131	Notch3	notch 3
1430724_at	-4.17	-4.63	-4.40	4.81E-11	71932	Ephx3	epoxide hydrolase 3
1420444_at	-4.28	-4.46	-4.37	1.42E-08	20519	Slc22a3	solute carrier family 22 (organic cation transporter), member 3
1422710_a_at	-3.71	-4.74	-4.22	8.33E-09	58226	Cacna1h	calcium channel, voltage-dependent, T type, alpha 1H subunit
1447517_at	-3.94	-3.47	-3.71	3.62E-05	72198	Skiv2l2	superkiller viralicidic activity 2-like 2 (S. cerevisiae)
1422028_a_at	-3.58	-3.80	-3.69	1.15E-09	23871	Ets1	E26 avian leukemia oncogene 1, 5' domain
1447657_s_at	-3.08	-4.28	-3.68	1.57E-07	68760	Synpo2l	synaptopodin 2-like
1429308_at	-3.97	-3.28	-3.62	3.16E-05	70673	Prdm16	PR domain containing 16
1433793_s_at	-3.78	-3.37	-3.57	6.59E-09	60345	Nrip2	nuclear receptor interacting protein 2
1420391_at	-3.81	-3.31	-3.56	2.24E-07	93742	Pard3	par-3 (partitioning defective 3) homolog (C. elegans)
1425521_at	-3.40	-3.56	-3.48	1.20E-07	218693	Paip1	polyadenylate binding protein-interacting protein 1
1424041_s_at	-3.42	-3.30	-3.36	5.38E-09	50908	C1s	complement component 1, s subcomponent
1415994_at	-3.15	-3.53	-3.34	1.25E-05	13106	Cyp2e1	cytochrome P450, family 2, subfamily e, polypeptide 1
1438636_s_at	-3.21	-3.45	-3.33	1.45E-06	382111	Susd5	sushi domain containing 5
1422027_a_at	-2.79	-3.70	-3.24	8.99E-08	23871	Ets1	E26 avian leukemia oncogene 1, 5' domain
1459253_at	-2.64	-3.74	-3.19	2.53E-07	69442	1700023H06Rik	RIKEN cDNA 1700023H06 gene
1426417_at	-3.11	-2.67	-2.89	2.17E-06	67864	Yipf4	Yip1 domain family, member 4
1422529_s_at	-3.26	-2.51	-2.88	8.14E-08	12373	Casq2	calsequestrin 2
1440021_at	-2.69	-2.88	-2.79	1.57E-07	239530	Gpr20	G protein-coupled receptor 20
1450952_at	-2.71	-2.83	-2.77	1.66E-08	18821	Pln	phospholamban
1419117_at	-2.77	-2.71	-2.74	1.14E-07	20518	Slc22a2	solute carrier family 22 (organic cation transporter), member 2
1434802_s_at	-3.21	-2.26	-2.74	3.10E-07	18205	Ntf3	neurotrophin 3
1436867_at	-2.59	-2.86	-2.72	2.48E-08	106393	Srl	sarcalumenin
1423359_at	-2.56	-2.88	-2.72	5.04E-07	18821	Pln	phospholamban
1437387_at	-2.48	-2.90	-2.69	2.86E-05	382111	Susd5	sushi domain containing 5
1430802_at	-2.98	-2.40	-2.69	0.006532242	15016	H2-Q5	histocompatibility 2, Q region locus 5
1460028_at	-2.39	-2.79	-2.59	2.62E-08	243547	Grip2	glutamate receptor interacting protein 2
1442077_at	-2.63	-2.53	-2.58	1.87E-07	76963	2310076G05Rik	RIKEN cDNA 2310076G05 gene
1448468_a_at	-2.43	-2.69	-2.56	2.91E-08	16497	Kcnab1	potassium voltage-gated channel, shaker-related subfamily, beta member 1
1424045_at	-2.69	-2.40	-2.55	7.33E-08	70544	Tmem242	transmembrane protein 242
1460458_at	-2.39	-2.55	-2.47	6.13E-07	78892	Crispld2	cysteine-rich secretory protein LCCL domain containing 2
1433783_at	-2.47	-2.45	-2.46	9.53E-06	24131	Ldb3	LIM domain binding 3
1417236_at	-2.29	-2.62	-2.46	1.28E-06	57440	Ehd3	EH-domain containing 3
1457132_at	-2.06	-2.83	-2.45	0.00043738	278795	Lrrc10b	leucine rich repeat containing 10B
1418485_at	-2.52	-2.37	-2.45	4.37E-09	20536	Slc4a3	solute carrier family 4 (anion exchanger), member 3
1423222_at	-2.42	-2.43	-2.43	1.65E-08	67252	Cap2	CAP, adenylate cyclase-associated protein, 2 (yeast)
1428948_at	-2.02	-2.76	-2.39	2.41E-07	16531	Kcnma1	potassium large conductance calcium-activated channel, subfamily M, alpha member 1
1433792_at	-2.34	-2.44	-2.39	5.40E-09	60345	Nrip2	nuclear receptor interacting protein 2
1449356_at	-2.08	-2.64	-2.36	4.72E-06	76294	Asb5	ankyrin repeat and SOCs box-containing 5
1441955_s_at	-2.32	-2.40	-2.36	3.36E-05	218693	Paip1	polyadenylate binding protein-interacting protein 1
1418744_s_at	-2.24	-2.44	-2.34	2.24E-06	57816	Tesc	tescalcin
1417917_at	-2.22	-2.45	-2.33	0.000137054	12797	Cnn1	calponin 1
1453152_at	-2.61	-2.06	-2.33	1.61E-07	71738	Mamdc2	MAM domain containing 2
1435998_at	-2.00	-2.64	-2.32	0.002503498	239083	Ccnb1ip1	cyclin B1 interacting protein 1
1447655_x_at	-2.39	-2.24	-2.31	2.49E-11	20679	Sox6	SRY-box containing gene 6
1434758_at	-2.18	-2.42	-2.30	5.05E-07	78892	Crispld2	cysteine-rich secretory protein LCCL domain containing 2
1460332_at	-2.23	-2.33	-2.28	2.62E-08	18821	Pln	phospholamban
1435378_at	-2.26	-2.30	-2.28	2.27E-05	66528	Smim5	small integral membrane protein 5
1418156_at	-2.46	-1.98	-2.22	5.25E-08	57814	Kcne4	potassium voltage-gated channel, Isk-related subfamily, gene 4
1430519_a_at	-2.49	-1.75	-2.12	3.44E-06	18983	Cnot7	CCR4-NOT transcription complex, subunit 7
1437127_at	-1.95	-2.25	-2.10	6.05E-07	240041	Zfp945	zinc finger protein 945
1437056_x_at	-2.15	-2.04	-2.09	1.64E-07	78892	Crispld2	cysteine-rich secretory protein LCCL domain containing 2
1438989_s_at	-2.11	-2.07	-2.09	2.13E-07	320860	B130021B11Rik	RIKEN cDNA B130021B11 gene
1457359_at	-1.78	-2.37	-2.07	0.000415763	234515	Inpp4b	inositol polyphosphate-4-phosphatase, type II
1442063_at	-2.37	-1.72	-2.05	1.30E-06	77739	Adamtsl1	ADAMTS-like 1
1452456_at	-2.08	-1.98	-2.03	1.16E-08	60345	Nrip2	nuclear receptor interacting protein 2
1442917_at	-1.73	-2.23	-1.98	2.25E-06	100040792	Gm11627	predicted gene 11627
1455444_at	-2.65	-1.28	-1.97	0.002855389	14395	Gabra2	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 2
1437429_at	-2.18	-1.66	-1.92	7.40E-08	77739	Adamtsl1	ADAMTS-like 1
1428444_at	-1.44	-2.33	-1.89	3.83E-06	65256	Asb2	ankyrin repeat and SOCS box-containing 2
1440534_at	-1.86	-1.85	-1.85	7.50E-09	381310	6330403A02Rik	RIKEN cDNA 6330403A02 gene
1422545_at	-1.94	-1.74	-1.84	3.97E-07	21385	Tbx2	T-box 2
1422644_at	-1.87	-1.80	-1.83	1.08E-05	50795	Sh3bgr	SH3-binding domain glutamic acid-rich protein

1451691_at	-1.76	-1.82	-1.79	5.52E-06	13617	Ednra	endothelin receptor type A
1449945_at	-1.75	-1.83	-1.79	7.03E-06	170826	Ppargc1b	peroxisome proliferative activated receptor, gamma, coactivator 1 beta
1432073_at	-1.98	-1.52	-1.75	9.81E-05	69684	Aarsd1	alanyl-tRNA synthetase domain containing 1
1432073_at	-1.98	-1.52	-1.75	9.81E-05	73635	Ptges3l	prostaglandin E synthase 3 (cytosolic)-like
1419220_at	-0.86	-2.64	-1.75	0.001184216	22437	Xirp1	xin actin-binding repeat containing 1
1460248_at	-1.81	-1.68	-1.74	7.53E-05	55987	Cpxm2	carboxypeptidase X 2 (M14 family)
1419741_at	-1.69	-1.79	-1.74	1.98E-09	114741	Supt16	suppressor of Ty 16
1448962_at	-1.70	-1.78	-1.74	9.57E-08	17880	Myh11	myosin, heavy polypeptide 11, smooth muscle
1424008_a_at	-1.79	-1.68	-1.73	7.89E-08	100041680	Gm3470	predicted gene 3470
1424008_a_at	-1.79	-1.68	-1.73	7.89E-08	71973	Rbpms2	RNA binding protein with multiple splicing 2
1426571_at	-1.89	-1.57	-1.73	1.99E-06	101772	Ano1	anoctamin 1, calcium activated chloride channel
1437820_at	-1.44	-1.99	-1.71	1.93E-05	14239	Foxs1	forkhead box S1
1428891_at	-1.68	-1.74	-1.71	7.67E-08	231440	Parm1	prostate androgen-regulated mucin-like protein 1
1455361_at	-1.65	-1.75	-1.70	3.59E-08	217480	Dgkb	diacylglycerol kinase, beta
1428549_at	-1.68	-1.70	-1.69	1.93E-07	74186	Ccdc3	coiled-coil domain containing 3
1446303_at	-1.68	-1.69	-1.68	0.011229188	16001	Igf1r	insulin-like growth factor I receptor
1424214_at	-1.62	-1.73	-1.68	8.77E-08	231440	Parm1	prostate androgen-regulated mucin-like protein 1
1418517_at	-1.71	-1.64	-1.67	0.000117328	16373	Irx3	Iroquois related homeobox 3 (Drosophila)
1460245_at	-1.82	-1.50	-1.66	8.47E-05	16643	Klrd1	killer cell lectin-like receptor, subfamily D, member 1
1433825_at	-1.59	-1.73	-1.66	3.44E-06	18213	Ntrk3	neurotrophic tyrosine kinase, receptor, type 3
1434786_at	-1.61	-1.70	-1.66	1.65E-07	329251	Ppp1r12b	protein phosphatase 1, regulatory (inhibitor) subunit 12B
1431007_at	-1.66	-1.64	-1.65	2.97E-08	100041621	Gm3435	predicted gene 3435
1431007_at	-1.66	-1.64	-1.65	2.97E-08	381062	2210404J11Rik	RIKEN cDNA 2210404J11 gene
1431007_at	-1.66	-1.64	-1.65	2.97E-08	100041574	9030025P20Rik	RIKEN cDNA 9030025P20 gene
1425978_at	-1.41	-1.88	-1.65	1.04E-05	214384	Myocd	myocardin
1426511_at	-1.35	-1.90	-1.63	5.08E-05	71733	Susd2	sushi domain containing 2
1427677_a_at	-1.60	-1.65	-1.62	6.45E-07	20679	Sox6	SRY-box containing gene 6
1439373_x_at	-1.57	-1.65	-1.61	3.73E-05	22419	Wnt5b	wingless-related MMTV integration site 5B
1421400_at	-1.72	-1.48	-1.60	3.44E-06	16533	Kcnmb1	potassium large conductance calcium-activated channel, subfamily M, beta member 1
1437150_at	-1.32	-1.85	-1.58	7.04E-06	242297	Fam110b	family with sequence similarity 110, member B
1449396_at	-1.65	-1.49	-1.57	1.71E-09	11754	Aoc3	amine oxidase, copper containing 3
1420533_at	-1.42	-1.69	-1.56	7.63E-06	60596	Gucy1a3	guanylate cyclase 1, soluble, alpha 3
1455262_at	-1.15	-1.94	-1.54	9.62E-05	207596	Thsd4	thrombospondin, type I, domain containing 4
1434008_at	-1.21	-1.85	-1.53	0.000572839	399548	Scn4b	sodium channel, type IV, beta
1437558_at	-1.36	-1.70	-1.53	6.92E-07	320860	B130021B11Rik	RIKEN cDNA B130021B11 gene
1454752_at	-1.52	-1.53	-1.53	8.68E-07	666794	Rbm24	RNA binding motif protein 24
1423495_at	-1.38	-1.64	-1.51	7.08E-09	26378	Decr2	2-4-dienoyl-Coenzyme A reductase 2, peroxisomal
1418393_a_at	-1.58	-1.41	-1.50	2.37E-08	16404	Itga7	integrin alpha 7
1429133_at	-1.31	-1.68	-1.49	9.88E-05	75124	Nxnl2	nucleoredoxin-like 2
1450910_at	-1.46	-1.52	-1.49	1.00E-06	67252	Cap2	CAP, adenylate cyclase-associated protein, 2 (yeast)
1418536_at	-1.57	-1.38	-1.48	0.01467538	15018	H2-Q7	histocompatibility 2, Q region locus 7
1418536_at	-1.57	-1.38	-1.48	0.01467538	15019	H2-Q8	histocompatibility 2, Q region locus 8
1418536_at	-1.57	-1.38	-1.48	0.01467538	68395	LOC68395	histocompatibility 2, Q region locus 6-like
1418536_at	-1.57	-1.38	-1.48	0.01467538	110558	H2-Q9	histocompatibility 2, Q region locus 9
1419075_s_at	-1.07	-1.87	-1.47	0.000118665	20209	Saa2	serum amyloid A 2
1419075_s_at	-1.07	-1.87	-1.47	0.000118665	20208	Saa1	serum amyloid A 1
1450869_at	-1.37	-1.55	-1.46	3.47E-06	14164	Fgf1	fibroblast growth factor 1
1422245_a_at	-1.52	-1.40	-1.46	8.25E-08	17540	Mrvi1	MRV integration site 1
1418534_at	-1.68	-1.24	-1.46	3.36E-05	57265	Fzd2	frizzled homolog 2 (Drosophila)
1435730_at	-1.55	-1.35	-1.45	1.11E-05	619317	D930026N18Rik	RIKEN cDNA D930026N18 gene
1450397_at	-1.46	-1.44	-1.45	1.32E-06	17755	Map1b	microtubule-associated protein 1B
1436566_at	-1.50	-1.40	-1.45	1.89E-07	217371	Rab40b	Rab40b, member RAS oncogene family
1420693_at	-1.49	-1.39	-1.44	7.31E-08	17929	Myom1	myomesin 1
1428519_at	-1.46	-1.40	-1.43	1.99E-08	66497	Cmss1	cms small ribosomal subunit 1
1425028_a_at	-1.40	-1.46	-1.43	3.79E-06	22004	Tpm2	tropomyosin 2, beta
1436155_at	-1.20	-1.64	-1.42	0.00010163	226518	Nmnat2	nicotinamide nucleotide adenylyltransferase 2
1434905_at	-1.55	-1.29	-1.42	3.72E-06	407790	Ndufa4l2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2
1439332_at	-1.49	-1.34	-1.41	8.53E-08	73284	Ddit4l	DNA-damage-inducible transcript 4-like
1443745_s_at	-2.71	-0.11	-1.41	0.014921623	13406	Dmp1	dentin matrix protein 1
1455271_at	-1.37	-1.45	-1.41	2.67E-06	620695	Gm13889	predicted gene 13889
1452707_at	-1.53	-1.28	-1.41	0.000236401	70788	Klhl30	kelch-like 30
1421855_at	-1.40	-1.35	-1.38	0.000119486	14190	Fgl2	fibrinogen-like protein 2
1419434_at	-1.63	-1.12	-1.38	8.60E-05	170441	Slc2a10	solute carrier family 2 (facilitated glucose transporter), member 10
1456621_at	-1.28	-1.48	-1.38	0.001250512	58909	Fam13a	family with sequence similarity 13, member A
1437173_at	-1.36	-1.38	-1.37	4.68E-09	13610	S1pr3	sphingosine-1-phosphate receptor 3
1434575_at	-0.88	-1.82	-1.35	8.15E-05	13821	Epb4.1l1	erythrocyte protein band 4.1-like 1
1422890_at	-1.36	-1.34	-1.35	2.02E-05	73173	Pcdh18	protocadherin 18
1459713_s_at	-1.50	-1.20	-1.35	6.16E-09	101772	Ano1	anoctamin 1, calcium activated chloride channel
1418471_at	-1.37	-1.32	-1.34	7.77E-07	18654	Pgf	placental growth factor
1459665_s_at	-1.39	-1.27	-1.33	9.13E-08	17540	Mrvi1	MRV integration site 1
1427485_at	-1.38	-1.28	-1.33	3.60E-05	93689	Lmod1	leiomodin 1 (smooth muscle)
1418755_at	-1.25	-1.40	-1.32	2.27E-05	21384	Tbx15	T-box 15
1435909_at	-1.43	-1.20	-1.32	0.001905894	77533	C030034I22Rik	RIKEN cDNA C030034I22 gene
1443746_x_at	-2.48	-0.15	-1.32	0.011113764	13406	Dmp1	dentin matrix protein 1
1452947_at	-1.33	-1.30	-1.31	5.55E-05	70355	Gprc5c	G protein-coupled receptor, family C, group 5, member C
1422554_at	-1.24	-1.39	-1.31	0.003401096	66647	Ndnl2	necdin-like 2
1437559_at	-1.29	-1.33	-1.31	8.04E-08	52882	Rgs7bp	regulator of G-protein signalling 7 binding protein

1433768_at	-1.23	-1.38	-1.31	1.73E-05	72333	Palld	palladin, cytoskeletal associated protein
1437936_at	-1.42	-1.19	-1.30	6.13E-07	434778	Ccdc160	coiled-coil domain containing 160
1439172_at	-1.39	-1.18	-1.29	8.04E-07	268878	Atp13a5	ATPase type 13A5
1427228_at	-1.32	-1.24	-1.28	5.27E-06	72333	Palld	palladin, cytoskeletal associated protein
1447863_s_at	-1.26	-1.30	-1.28	0.000100708	18227	Nr4a2	nuclear receptor subfamily 4, group A, member 2
1416770_at	-1.25	-1.30	-1.27	0.012913469	59041	Stk25	serine/threonine kinase 25 (yeast)
1435339_at	-1.27	-1.26	-1.27	1.61E-08	233107	Kctd15	potassium channel tetramerisation domain containing 15
1419109_at	-0.94	-1.57	-1.26	2.07E-05	15464	Hrc	histidine rich calcium binding protein
1417253_at	-1.20	-1.31	-1.25	1.56E-09	14300	Frg1	FSHD region gene 1
1426416_a_at	-1.10	-1.40	-1.25	5.60E-06	67864	Yipf4	Yip1 domain family, member 4
1436876_at	-1.22	-1.29	-1.25	4.58E-08	52882	Rgs7bp	regulator of G-protein signalling 7 binding protein
1429027_at	-1.33	-1.16	-1.25	1.67E-07	100616095	0610007N19Rik	RIKEN cDNA 0610007N19
1420534_at	-1.03	-1.47	-1.25	9.34E-06	60596	Gucy1a3	guanylate cyclase 1, soluble, alpha 3
1452474_a_at	-1.43	-1.06	-1.24	9.85E-08	109979	Art3	ADP-ribosyltransferase 3
1448649_at	-1.35	-1.13	-1.24	1.13E-07	13809	Enpep	glutamyl aminopeptidase
1436080_at	-1.23	-1.24	-1.23	3.78E-05	100382	AW011738	expressed sequence AW011738
1423136_at	-1.32	-1.15	-1.23	7.60E-06	14164	Fgf1	fibroblast growth factor 1
1440009_at	-1.15	-1.31	-1.23	4.47E-05	170639	Olfr78	olfactory receptor 78
1418532_at	-0.99	-1.46	-1.23	0.0001868	57265	Fzd2	frizzled homolog 2 (Drosophila)
1420877_at	-1.06	-1.39	-1.23	6.67E-05	56526	06-Sep	septin 6
1422860_at	-1.76	-0.69	-1.23	0.000491084	67405	Nts	neurotensin
1447260_at	-1.27	-1.18	-1.23	4.60E-06	15007	H2-Q10	histocompatibility 2, Q region locus 10
1447260_at	-1.27	-1.18	-1.23	4.60E-06	667977	Gm8909	predicted gene 8909
1447260_at	-1.27	-1.18	-1.23	4.60E-06	69717	Gm10499	predicted gene 10499
1440859_at	-1.55	-0.89	-1.22	6.02E-05	238161	Akap6	A kinase (PRKA) anchor protein 6
1429313_at	-1.41	-1.03	-1.22	6.17E-06	26563	Ror1	receptor tyrosine kinase-like orphan receptor 1
1424254_at	-1.15	-1.29	-1.22	0.000503714	68713	Ifitm1	interferon induced transmembrane protein 1
1417985_at	-1.07	-1.36	-1.22	1.29E-05	67122	Nrarp	Notch-regulated ankyrin repeat protein
1423566_a_at	-1.10	-1.33	-1.21	0.003041763	15505	Hsph1	heat shock 105kDa/110kDa protein 1
1453473_a_at	-1.33	-1.08	-1.21	6.94E-08	100040531	Dynlt1f	dynein light chain Tctex-type 1F
1453473_a_at	-1.33	-1.08	-1.21	6.94E-08	21648	Dynlt1b	dynein light chain Tctex-type 1B
1453473_a_at	-1.33	-1.08	-1.21	6.94E-08	100040563	Dynlt1c	dynein light chain Tctex-type 1C
1453473_a_at	-1.33	-1.08	-1.21	6.94E-08	100310872	Dynlt1a	dynein light chain Tctex-type 1A
1417701_at	-1.16	-1.25	-1.20	0.000138525	76142	Ppp1r14c	protein phosphatase 1, regulatory (inhibitor) subunit 14c
1435399_at	-1.05	-1.33	-1.19	2.44E-06	118449	Synpo2	synaptopodin 2
1428454_at	-1.18	-1.18	-1.18	2.25E-08	192197	Bcas3	breast carcinoma amplified sequence 3
1438031_at	-1.15	-1.20	-1.18	0.003555772	240168	Rasgrp3	RAS, guanyl releasing protein 3
1418106_at	-1.13	-1.22	-1.17	1.84E-07	15214	Hey2	hairy/enhancer-of-split related with YRPW motif 2
1426569_a_at	-1.22	-1.12	-1.17	0.000814063	14302	Frk	fyn-related kinase
1419816_s_at	-0.85	-1.49	-1.17	0.000235303	74155	Errfi1	ERBB receptor feedback inhibitor 1
1429013_at	-1.27	-1.05	-1.16	7.78E-07	78283	Map7d2	MAP7 domain containing 2
1454867_at	-1.16	-1.16	-1.16	6.05E-06	433938	Mn1	meningioma 1
1433525_at	-1.34	-0.98	-1.16	3.31E-06	13617	Ednra	endothelin receptor type A
1419738_a_at	-1.10	-1.21	-1.15	6.11E-07	22004	Tpm2	tropomyosin 2, beta
1428538_s_at	-1.44	-0.86	-1.15	5.31E-05	71660	Rarres2	retinoic acid receptor responder (tazarotene induced) 2
1417305_at	-1.05	-1.24	-1.15	1.02E-05	11790	Speg	SPEG complex locus
1434776_at	-1.12	-1.16	-1.14	0.000516987	20356	Sema5a	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A
1451644_a_at	-1.14	-1.13	-1.14	0.039093044	15015	H2-Q4	histocompatibility 2, Q region locus 4
1451644_a_at	-1.14	-1.13	-1.14	0.039093044	68395	LOC68395	histocompatibility 2, Q region locus 6-like
1451644_a_at	-1.14	-1.13	-1.14	0.039093044	110557	H2-Q6	histocompatibility 2, Q region locus 6
1431008_at	-1.11	-1.15	-1.13	0.016811327	110557	H2-Q6	histocompatibility 2, Q region locus 6
1431008_at	-1.11	-1.15	-1.13	0.016811327	68395	LOC68395	histocompatibility 2, Q region locus 6-like
1425191_at	-1.21	-1.05	-1.13	0.028570441	77090	Ocel1	occludin/ELL domain containing 1
1427271_at	-1.07	-1.18	-1.13	9.30E-08	235132	Zbtb44	zinc finger and BTB domain containing 44
1455636_at	-1.80	-0.46	-1.13	0.005233716	268890	Lsamp	limbic system-associated membrane protein
1449178_at	-1.12	-1.13	-1.13	1.36E-05	53318	Pdlim3	PDZ and LIM domain 3
1444139_at	-1.17	-1.08	-1.13	3.72E-08	73284	Ddit4l	DNA-damage-inducible transcript 4-like
1434943_at	-1.14	-1.11	-1.12	0.015170696	226123	Morn4	MORN repeat containing 4
1452388_at	-1.29	-0.95	-1.12	0.001141033	193740	Hspa1a	heat shock protein 1A
1455743_at	-0.91	-1.33	-1.12	0.00064873	241327	Olfml2a	olfactomedin-like 2A
1434171_at	-1.13	-1.11	-1.12	0.004337875	238692	Zfp874a	zinc finger protein 874a
1422602_a_at	-0.98	-1.26	-1.12	0.000143276	22419	Wnt5b	wingless-related MMTV integration site 5B
1452399_at	-1.16	-1.08	-1.12	0.001164316	50779	Rgs6	regulator of G-protein signaling 6
1434141_at	-1.23	-1.00	-1.11	1.24E-07	60596	Gucy1a3	guanylate cyclase 1, soluble, alpha 3
1436134_at	-1.02	-1.21	-1.11	2.85E-05	72821	Scn2b	sodium channel, voltage-gated, type II, beta
1439475_at	-1.05	-1.18	-1.11	0.003905626	72807	Zfp429	zinc finger protein 429
1453087_at	-1.19	-1.04	-1.11	3.05E-07	70744	6330403L08Rik	RIKEN cDNA 6330403L08 gene
1438658_a_at	-1.17	-1.03	-1.10	8.62E-09	13610	S1pr3	sphingosine-1-phosphate receptor 3
1436119_at	-1.01	-1.18	-1.10	0.000108719	216188	Aldh1l2	aldehyde dehydrogenase 1 family, member L2
1438271_at	-1.14	-1.02	-1.08	0.000293399	210126	Lpp	LIM domain containing preferred translocation partner in lipoma
1423180_at	-0.63	-1.53	-1.08	0.002077364	16500	Kcnb1	potassium voltage gated channel, Shab-related subfamily, member 1
1451751_at	-1.14	-1.01	-1.08	6.31E-07	73284	Ddit4l	DNA-damage-inducible transcript 4-like
1428384_at	-1.19	-0.96	-1.07	1.81E-06	52829	Lurap1l	leucine rich adaptor protein 1-like
1417455_at	-0.98	-1.17	-1.07	1.17E-05	21809	Tgfb3	transforming growth factor, beta 3
1455237_at	-1.03	-1.11	-1.07	1.26E-10	72344	Usp36	ubiquitin specific peptidase 36
1453855_at	-1.24	-0.90	-1.07	7.18E-06	67622	Mxra7	matrix-remodelling associated 7

1428067_at	-1.04	-1.11	-1.07	1.05E-06	70784	Rasl12	RAS-like, family 12
1438288_x_at	-1.08	-1.06	-1.07	0.003920521	68786	1110059G02Rik	RIKEN cDNA 1110059G02 gene
1455404_at	-0.77	-1.37	-1.07	0.000124569	59091	Jph2	junctophilin 2
1425341_at	-1.07	-1.06	-1.07	0.000378469	16527	Kcnk3	potassium channel, subfamily K, member 3
1444105_at	-1.00	-1.13	-1.07	0.001025289	11475	Acta2	actin, alpha 2, smooth muscle, aorta
1428896_at	-1.15	-0.96	-1.05	2.60E-05	68797	Pdgfrl	platelet-derived growth factor receptor-like
1416505_at	-1.42	-0.68	-1.05	0.005256069	15370	Nr4a1	nuclear receptor subfamily 4, group A, member 1
1423854_a_at	-1.15	-0.95	-1.05	2.23E-05	68939	Rasl11b	RAS-like, family 11, member B
1446400_at	-0.83	-1.26	-1.05	0.000238522	259097	Olfr558	olfactory receptor 558
1418601_at	-1.35	-0.74	-1.04	0.006750786	26358	Aldh1a7	aldehyde dehydrogenase family 1, subfamily A7
1418467_at	-1.18	-0.91	-1.04	5.57E-06	66993	Smarcd3	member 3
1424896_at	-1.28	-0.81	-1.04	9.04E-05	64450	Gpr85	G protein-coupled receptor 85
1434680_at	-0.79	-1.29	-1.04	0.00015352	263406	Plekhg3	pleckstrin homology domain containing, family G (with RhoGef domain) member 3
1436411_at	-1.20	-0.88	-1.04	6.49E-06	268878	Atp13a5	ATPase type 13A5
1448443_at	-1.18	-0.89	-1.04	2.43E-06	20713	Serpini1	serine (or cysteine) peptidase inhibitor, clade I, member 1
1425505_at	-0.86	-1.20	-1.03	0.000253317	107589	Mylk	myosin, light polypeptide kinase
1421471_at	-1.21	-0.84	-1.02	3.93E-05	18166	Npy1r	neuropeptide Y receptor Y1
1457473_at	-0.98	-1.06	-1.02	4.83E-06	12648	Chd1	chromodomain helicase DNA binding protein 1
1441926_x_at	-0.83	-1.20	-1.02	0.001567113	20776	Tmie	transmembrane inner ear
1417986_at	-0.72	-1.31	-1.02	0.000129635	67122	Nrarp	Notch-regulated ankyrin repeat protein
1422473_at	-1.05	-0.98	-1.02	0.001694977	18578	Pde4b	phosphodiesterase 4B, cAMP specific
1416702_at	-1.06	-0.97	-1.02	2.57E-07	20713	Serpini1	serine (or cysteine) peptidase inhibitor, clade I, member 1
1421854_at	-1.07	-0.95	-1.01	0.003650214	14190	Fgl2	fibrinogen-like protein 2
1437902_s_at	-1.30	-0.72	-1.01	2.08E-05	71660	Rarres2	retinoic acid receptor responder (tazarotene induced) 2
1426855_at	-1.15	-0.86	-1.01	0.000155467	52666	Arhgef25	Rho guanine nucleotide exchange factor (GEF) 25
1437330_at	-1.69	-0.32	-1.01	0.003021503	233328	Lrrk1	leucine-rich repeat kinase 1
1428116_a_at	-1.04	-0.97	-1.00	2.87E-07	100040563	Dynlt1c	dynein light chain Tctex-type 1C
1428116_a_at	-1.04	-0.97	-1.00	2.87E-07	100040531	Dynlt1f	dynein light chain Tctex-type 1F
1428116_a_at	-1.04	-0.97	-1.00	2.87E-07	21648	Dynlt1b	dynein light chain Tctex-type 1B
1428116_a_at	-1.04	-0.97	-1.00	2.87E-07	100310872	Dynlt1a	dynein light chain Tctex-type 1A
1434918_at	-0.61	-1.39	-1.00	0.024570938	20679	Sox6	SRY-box containing gene 6
1442325_at	-0.94	-1.04	-0.99	0.000435604	224617	Tbc1d24	TBC1 domain family, member 24
1436413_at	-1.03	-0.95	-0.99	6.68E-05	14302	Frk	fyn-related kinase
1437247_at	-0.97	-1.01	-0.99	7.59E-05	14284	Fosl2	fos-like antigen 2
1452670_at	-1.01	-0.97	-0.99	1.06E-06	98932	Myl9	myosin, light polypeptide 9, regulatory
1416846_a_at	-1.03	-0.94	-0.99	8.79E-05	55983	Pdzrn3	PDZ domain containing RING finger 3
1455535_at	-1.05	-0.92	-0.98	2.98E-05	20678	Sox5	SRY-box containing gene 5
1426858_at	-0.99	-0.97	-0.98	9.10E-05	16324	Inhbb	inhibin beta-B
1425993_a_at	-0.83	-1.12	-0.98	0.006306749	15505	Hsph1	heat shock 105kDa/110kDa protein 1
1447853_x_at	-1.03	-0.93	-0.98	0.000111674	16553	Kif13a	kinesin family member 13A
1418876_at	-1.18	-0.78	-0.98	3.52E-06	15229	Foxd1	forkhead box D1
1440475_at	-0.95	-1.01	-0.98	1.45E-05	100382	AW011738	expressed sequence AW011738
1456793_at	-0.83	-1.11	-0.97	0.001410625	231162	Cytl1	cytokine-like 1
1452163_at	-0.92	-1.02	-0.97	4.27E-06	23871	Ets1	E26 avian leukemia oncogene 1, 5' domain
1434601_at	-0.88	-1.06	-0.97	0.000465493	105827	Amigo2	adhesion molecule with Ig like domain 2
1452365_at	-1.07	-0.87	-0.97	0.000209837	234356	Csgalnact1	chondroitin sulfate N-acetylgalactosaminyltransferase 1
1427126_at	-1.27	-0.66	-0.97	0.003175368	15511	Hspa1b	heat shock protein 1B
1452308_a_at	-0.95	-0.96	-0.96	0.002749936	98660	Atp1a2	ATPase, Na+/K+ transporting, alpha 2 polypeptide
1449002_at	-0.81	-1.11	-0.96	0.000995942	27280	Phlda3	pleckstrin homology-like domain, family A, member 3
1457776_at	-1.08	-0.82	-0.95	0.005017356	52145	D9Ertd720e	DNA segment, Chr 9, ERATO Doi 720, expressed
1457776_at	-1.08	-0.82	-0.95	0.005017356	72560	Naalad2	N-acetylated alpha-linked acidic dipeptidase 2
1450750_a_at	-1.01	-0.89	-0.95	0.000474665	18227	Nr4a2	nuclear receptor subfamily 4, group A, member 2
1449363_at	-1.10	-0.80	-0.95	0.000100393	11910	Atf3	activating transcription factor 3
1455629_at	-0.80	-1.10	-0.95	0.000878763	13488	Drd1a	dopamine receptor D1A
1416700_at	-1.00	-0.90	-0.95	0.001041827	74194	Rnd3	Rho family GTPase 3
1436233_at	-1.20	-0.70	-0.95	0.000247827	237754	Btnl9	butyrophilin-like 9
1435649_at	-0.95	-0.94	-0.95	6.11E-07	68810	Nexn	nexilin
1416129_at	-0.81	-1.08	-0.94	6.22E-06	74155	Errfi1	ERBB receptor feedback inhibitor 1
1422631_at	-1.00	-0.88	-0.94	5.20E-05	11622	Ahr	aryl-hydrocarbon receptor
1452398_at	-1.04	-0.84	-0.94	6.64E-06	74055	Plce1	phospholipase C, epsilon 1
1448598_at	-0.92	-0.96	-0.94	0.000106884	23948	Mmp17	matrix metallopeptidase 17
1437618_x_at	-1.16	-0.72	-0.94	0.000252635	64450	Gpr85	G protein-coupled receptor 85
1437422_at	-0.85	-1.03	-0.94	0.000238854	20356	Sema5a	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A
1423505_at	-0.86	-1.02	-0.94	2.88E-05	21345	Tagln	transgelin
1418533_s_at	-0.93	-0.95	-0.94	0.005369694	57265	Fzd2	frizzled homolog 2 (Drosophila)
1431167_at	-0.99	-0.87	-0.93	6.67E-05	110197	Dgkg	diacylglycerol kinase, gamma
1417009_at	-0.89	-0.96	-0.92	0.000911414	50909	C1ra	complement component 1, r subcomponent A
1421826_at	-0.92	-0.93	-0.92	0.006284777	54485	Dll4	delta-like 4 (Drosophila)
1429888_a_at	-0.80	-1.04	-0.92	1.75E-06	69253	Hspb2	heat shock protein 2
1431020_a_at	-0.83	-1.01	-0.92	5.06E-05	67529	Fgfr1op2	FGFR1 oncogene partner 2
1450944_at	-1.01	-0.83	-0.92	7.53E-06	121021	Cspg4	chondroitin sulfate proteoglycan 4
1441881_x_at	-0.89	-0.94	-0.92	0.000169075	73121	Fam101a	family with sequence similarity 101, member A
1436329_at	-1.36	-0.47	-0.92	0.036972206	13655	Egr3	early growth response 3
1423319_at	-0.83	-1.00	-0.92	0.0055513	15242	Hhex	hematopoietically expressed homeobox
1426725_s_at	-0.90	-0.93	-0.92	0.000105491	23871	Ets1	E26 avian leukemia oncogene 1, 5' domain
1420871_at	-0.97	-0.86	-0.92	0.000298981	54195	Gucy1b3	guanylate cyclase 1, soluble, beta 3

1427127_x_at	-1.20	-0.62	-0.91	0.00275081	15511	Hspa1b	heat shock protein 1B
1416287_at	-0.89	-0.94	-0.91	2.95E-06	19736	Rgs4	regulator of G-protein signaling 4
1452361_at	-0.97	-0.84	-0.91	3.60E-05	109331	Rnf20	ring finger protein 20
1428864_at	-0.96	-0.85	-0.90	0.000733063	18218	Dusp8	dual specificity phosphatase 8
1419978_s_at	-0.94	-0.86	-0.90	1.51E-07	52666	Arhgef25	Rho guanine nucleotide exchange factor (GEF) 25
1416661_at	-0.66	-1.13	-0.90	0.000111036	13669	Eif3a	eukaryotic translation initiation factor 3, subunit A
1444422_at	-0.96	-0.83	-0.90	0.001253888	279653	Pcdh19	protocadherin 19
1435767_at	-0.98	-0.81	-0.89	0.002305401	235281	Scn3b	sodium channel, voltage-gated, type III, beta
1448664_a_at	-0.97	-0.82	-0.89	0.000938112	11790	Speg	SPEG complex locus
1417680_at	-0.74	-1.04	-0.89	0.00915078	16493	Kcna5	potassium voltage-gated channel, shaker-related subfamily, member 5
1433454_at	-0.77	-1.01	-0.89	5.08E-05	99382	Abtb2	ankyrin repeat and BTB (POZ) domain containing 2
1422134_at	-0.21	-1.57	-0.89	0.025705423	14282	Fosb	FBJ osteosarcoma oncogene B
1439364_a_at	-0.86	-0.91	-0.89	0.009277329	17390	Mmp2	matrix metallopeptidase 2
1422882_at	-0.80	-0.97	-0.89	0.000447855	19027	Sypl	synaptophysin-like protein
1423942_a_at	-0.86	-0.91	-0.89	0.000779168	12325	Camk2g	calcium/calmodulin-dependent protein kinase II gamma
1415812_at	-0.89	-0.88	-0.89	3.76E-05	227753	Gsn	gelsolin
1449860_at	-0.97	-0.80	-0.88	1.32E-06	75689	Higd1b	HIG1 domain family, member 1B
1421297_a_at	-0.89	-0.87	-0.88	5.81E-05	12288	Cacna1c	calcium channel, voltage-dependent, L type, alpha 1C subunit
1422905_s_at	-0.99	-0.78	-0.88	0.000490996	55990	Fmo2	flavin containing monooxygenase 2
1434944_at	-0.80	-0.96	-0.88	9.85E-05	13400	Dmpk	dystrophia myotonica-protein kinase
1422293_a_at	-0.89	-0.86	-0.88	0.006053569	106931	Kctd1	potassium channel tetramerisation domain containing 1
1416136_at	-0.77	-0.97	-0.87	0.011130222	17390	Mmp2	matrix metallopeptidase 2
1439014_at	-1.03	-0.72	-0.87	0.000103334	239796	Mb21d2	Mab-21 domain containing 2
1417012_at	-0.85	-0.90	-0.87	0.000917292	15529	Sdc2	syndecan 2
1422562_at	-0.73	-1.01	-0.87	1.27E-05	56437	Rrad	Ras-related associated with diabetes
1451340_at	-1.08	-0.66	-0.87	0.002066606	214855	Arid5a	AT rich interactive domain 5A (MRF1-like)
1418280_at	-1.17	-0.57	-0.87	0.004021234	23849	Klf6	Kruppel-like factor 6
1452368_at	-0.76	-0.97	-0.87	5.06E-07	110279	Bcr	breakpoint cluster region
1421827_at	-1.05	-0.68	-0.86	0.00381002	54485	Dll4	delta-like 4 (Drosophila)
1418086_at	-0.94	-0.79	-0.86	2.73E-05	68458	Ppp1r14a	protein phosphatase 1, regulatory (inhibitor) subunit 14A
1415877_at	-0.82	-0.91	-0.86	0.000100957	22240	Dpysl3	dihydropyrimidinase-like 3
1449584_at	-0.95	-0.77	-0.86	0.00172042	110197	Dgkg	diacylglycerol kinase, gamma
1417788_at	-0.78	-0.94	-0.86	1.94E-06	20618	Sncg	synuclein, gamma
1437928_at	-1.17	-0.55	-0.86	0.026204492	53601	Pcdh12	protocadherin 12
1434990_at	-0.89	-0.83	-0.86	4.39E-06	320472	Ppm1e	protein phosphatase 1E (PP2C domain containing)
1455034_at	-0.91	-0.81	-0.86	0.000471929	18227	Nr4a2	nuclear receptor subfamily 4, group A, member 2
1435987_x_at	-0.85	-0.86	-0.86	0.001557756	68786	1110059G02Rik	RIKEN cDNA 1110059G02 gene
1456735_x_at	-0.94	-0.77	-0.85	1.34E-05	235534	Acpl2	acid phosphatase-like 2
1418835_at	-0.92	-0.78	-0.85	9.10E-06	21664	Phlda1	pleckstrin homology-like domain, family A, member 1
1416652_at	-0.90	-0.80	-0.85	1.19E-05	66695	Aspn	asporin
1437834_s_at	-0.72	-0.97	-0.85	0.002488187	80708	Pacsin3	protein kinase C and casein kinase substrate in neurons 3
1419938_s_at	-0.97	-0.72	-0.85	0.00020597	207212	Arhgef17	Rho guanine nucleotide exchange factor (GEF) 17
1455851_at	-0.97	-0.72	-0.85	0.000557972	12160	Bmp5	bone morphogenetic protein 5
1439532_s_at	-0.78	-0.91	-0.84	0.011665383	16553	Kif13a	kinesin family member 13A
1448325_at	-0.88	-0.81	-0.84	5.39E-05	17872	Ppp1r15a	protein phosphatase 1, regulatory (inhibitor) subunit 15A
1431182_at	-0.76	-0.92	-0.84	5.13E-06	15481	Hspa8	heat shock protein 8
1448876_at	-0.74	-0.94	-0.84	0.000129963	59056	Evc	Ellis van Creveld gene syndrome
1452349_x_at	-1.09	-0.60	-0.84	0.008498605	381308	Mnda	myeloid cell nuclear differentiation antigen
1452349_x_at	-1.09	-0.60	-0.84	0.008498605	226695	Ifi205	interferon activated gene 205
1435703_at	-0.49	-1.18	-0.84	0.024928349	72828	Ubash3b	ubiquitin associated and SH3 domain containing, B
1447669_s_at	-0.97	-0.70	-0.84	0.000632056	14706	Gng4	guanine nucleotide binding protein (G protein), gamma 4
1418714_at	-0.87	-0.80	-0.84	0.000117765	18218	Dusp8	dual specificity phosphatase 8
1420699_at	-0.75	-0.92	-0.84	0.001089015	56644	Clec7a	C-type lectin domain family 7, member a
1425660_at	-0.86	-0.82	-0.84	8.33E-05	228662	Btbd3	BTB (POZ) domain containing 3
1456874_at	-0.78	-0.89	-0.84	0.00027304	399558	Flrt2	fibronectin leucine rich transmembrane protein 2
1436819_at	-0.81	-0.86	-0.83	0.000178671	56526	06-Sep	septin 6
1433682_at	-0.97	-0.70	-0.83	2.49E-05	207212	Arhgef17	Rho guanine nucleotide exchange factor (GEF) 17
1416039_x_at	-1.00	-0.67	-0.83	0.003173488	16007	Cyr61	cysteine rich protein 61
1450418_a_at	-0.73	-0.93	-0.83	5.28E-05	67864	Yipf4	Yip1 domain family, member 4
1418743_a_at	-0.61	-1.04	-0.83	0.003793184	57816	Tesc	tescalcin
1420872_at	-0.87	-0.77	-0.82	0.000280421	54195	Gucy1b3	guanylate cyclase 1, soluble, beta 3
1448747_at	-0.61	-1.04	-0.82	0.000238005	67731	Fbxo32	F-box protein 32
1436895_at	-0.74	-0.90	-0.82	0.005216932	212285	Arap2	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2
1438133_a_at	-0.90	-0.74	-0.82	0.008242047	16007	Cyr61	cysteine rich protein 61
1454973_at	-0.81	-0.82	-0.82	4.30E-07	54343	Atf7ip	activating transcription factor 7 interacting protein
1424733_at	-0.94	-0.69	-0.82	3.61E-05	140795	P2ry14	purinergic receptor P2Y, G-protein coupled, 14
1451612_at	-0.68	-0.95	-0.82	0.010315753	17748	Mt1	metallothionein 1
1436203_a_at	-1.01	-0.63	-0.82	0.000110338	68786	1110059G02Rik	RIKEN cDNA 1110059G02 gene
1422889_at	-0.85	-0.79	-0.82	4.92E-05	73173	Pcdh18	protocadherin 18
1455296_at	-0.74	-0.89	-0.82	5.74E-05	224129	Adcy5	adenylate cyclase 5
1449893_a_at	-0.88	-0.75	-0.81	7.78E-06	16206	Lrig1	leucine-rich repeats and immunoglobulin-like domains 1
1450803_at	-0.64	-0.99	-0.81	0.001044714	18205	Ntf3	neurotrophin 3
1453540_at	-0.63	-0.99	-0.81	0.010118138	74502	5430404G13Rik	RIKEN cDNA 5430404G13 gene
1435137_s_at	-0.92	-0.70	-0.81	9.51E-06	319269	A130040M12Rik	RIKEN cDNA A130040M12 gene
1435137_s_at	-0.92	-0.70	-0.81	9.51E-06	71739	1200015M12Rik	RIKEN cDNA 1200015M12 gene
1422474_at	-0.84	-0.77	-0.81	0.002370716	18578	Pde4b	phosphodiesterase 4B, cAMP specific
1434210_s_at	-0.80	-0.81	-0.80	6.35E-07	16206	Lrig1	leucine-rich repeats and immunoglobulin-like domains 1

1436861_at	-0.92	-0.68	-0.80	0.040897177	16196	Il7	interleukin 7
1430286_s_at	-0.79	-0.82	-0.80	2.04E-06	100043766	Gm14057	Ppp1r14c pseudogene
1430286_s_at	-0.79	-0.82	-0.80	2.04E-06	76142	Ppp1r14c	protein phosphatase 1, regulatory (inhibitor) subunit 14c
1432336_at	-0.80	-0.80	-0.80	0.010217331	114668	5033404E19Rik	NSA2 ribosome biogenesis homolog pseudogene
1436919_at	-1.01	-0.59	-0.80	0.000460264	277414	Trp53i11	transformation related protein 53 inducible protein 11
1440992_at	-0.81	-0.79	-0.80	9.91E-05	73229	3110052M02Rik	RIKEN cDNA 3110052M02 gene
1448140_at	-0.91	-0.68	-0.79	0.000363648	109006	Ciapin1	cytokine induced apoptosis inhibitor 1
1438886_at	-0.88	-0.71	-0.79	0.001917935	56198	Heyl	hairy/enhancer-of-split related with YRPW motif-like
1441792_at	-0.71	-0.88	-0.79	1.37E-05	240041	Zfp945	zinc finger protein 945
1440681_at	-0.64	-0.95	-0.79	0.004978564	11441	Chrna7	cholinergic receptor, nicotinic, alpha polypeptide 7
1430648_at	-0.65	-0.93	-0.79	0.016367384	72821	Scn2b	sodium channel, voltage-gated, type II, beta
1449311_at	-0.70	-0.88	-0.79	0.000106017	12013	Bach1	BTB and CNC homology 1
1437788_at	-0.71	-0.87	-0.79	0.00430879	83395	Sp6	trans-acting transcription factor 6
1436600_at	-0.88	-0.71	-0.79	0.000127702	244579	Tox3	TOX high mobility group box family member 3
1452348_s_at	-1.09	-0.49	-0.79	0.005355605	15951	Ifi204	interferon activated gene 204
1452348_s_at	-1.09	-0.49	-0.79	0.005355605	100040462	Mndal	myeloid nuclear differentiation antigen like
1452348_s_at	-1.09	-0.49	-0.79	0.005355605	381308	Mnda	myeloid cell nuclear differentiation antigen
1452348_s_at	-1.09	-0.49	-0.79	0.005355605	226695	Ifi205	interferon activated gene 205
1416081_at	-0.71	-0.87	-0.79	5.82E-05	17125	Smad1	SMAD family member 1
1417541_at	-0.98	-0.60	-0.79	0.005315341	15201	Hells	helicase, lymphoid specific
1437171_x_at	-0.83	-0.75	-0.79	7.51E-05	227753	Gsn	gelsolin
1455050_at	-0.95	-0.61	-0.78	3.31E-06	320736	Vstm4	V-set and transmembrane domain containing 4
1423341_at	-0.91	-0.66	-0.78	9.60E-05	121021	Cspg4	chondroitin sulfate proteoglycan 4
1429974_at	-0.84	-0.72	-0.78	8.38E-06	76365	Tbx18	T-box18
1460466_at	-0.79	-0.77	-0.78	0.000979121	100503822	LOC100503822	uncharacterized LOC100503822
1460466_at	-0.79	-0.77	-0.78	0.000979121	73385	Fam177a	family with sequence similarity 177, member A
1460466_at	-0.79	-0.77	-0.78	0.000979121	100101807	1700047I17Rik2	RIKEN cDNA 1700047I17 gene 2
1418341_at	-0.96	-0.59	-0.78	0.00215956	19341	Rab4a	RAB4A, member RAS oncogene family
1429030_at	-0.98	-0.58	-0.78	0.001088773	109323	C1qtnf7	C1q and tumor necrosis factor related protein 7
1457404_at	-0.84	-0.70	-0.77	0.001113197	80859	Nfkbiz	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, zeta
1427742_a_at	-0.81	-0.74	-0.77	3.49E-05	23849	Klf6	Kruppel-like factor 6
1422730_at	-0.77	-0.78	-0.77	2.08E-06	29806	Limd1	LIM domains containing 1
1436991_x_at	-0.89	-0.64	-0.77	0.000144181	227753	Gsn	gelsolin
1454613_at	-0.76	-0.77	-0.77	0.000494979	22240	Dpysl3	dihydropyrimidinase-like 3
1454613_at	-0.76	-0.77	-0.77	0.000494979	109253	9430041P20Rik	RIKEN cDNA 9430041P20 gene
1425491_at	-0.79	-0.74	-0.77	0.000127186	12166	Bmpr1a	bone morphogenetic protein receptor, type 1A
1445334_at	-0.97	-0.56	-0.76	0.00182231	73385	Fam177a	family with sequence similarity 177, member A
1445334_at	-0.97	-0.56	-0.76	0.00182231	100101807	1700047I17Rik2	RIKEN cDNA 1700047I17 gene 2
1445422_at	-0.74	-0.79	-0.76	0.024861995	621549	LOC621549	uncharacterized LOC621549
1451229_at	-0.82	-0.70	-0.76	6.22E-06	232232	Hdac11	histone deacetylase 11
1451342_at	-1.35	-0.18	-0.76	0.01169893	233744	Spon1	spondin 1, (f-spondin) extracellular matrix protein
1452318_a_at	-0.99	-0.53	-0.76	0.002695935	15511	Hspa1b	heat shock protein 1B
1458341_x_at	-0.76	-0.75	-0.76	7.11E-07	242202	Pde5a	phosphodiesterase 5A, cGMP-specific
1425828_at	-0.31	-1.19	-0.75	0.005916555	18096	Nkx6-1	NK6 homeobox 1
1425391_a_at	-0.51	-1.00	-0.75	0.003476259	79196	Osbpl5	oxysterol binding protein-like 5
1450651_at	-0.94	-0.56	-0.75	0.001226803	17909	Myo10	myosin X
1449280_at	-0.82	-0.68	-0.75	0.002282353	71690	Esm1	endothelial cell-specific molecule 1
1418216_at	-0.55	-0.95	-0.75	0.000100856	23887	Ggt5	gamma-glutamyltransferase 5
1418188_a_at	-0.65	-0.85	-0.75	1.75E-05	72289	Malat1	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)
1418188_a_at	-0.65	-0.85	-0.75	1.75E-05	54409	Ramp2	receptor (calcitonin) activity modifying protein 2
1448870_at	-0.73	-0.76	-0.74	0.000572329	268977	Ltbp1	latent transforming growth factor beta binding protein 1
1419302_at	-0.74	-0.75	-0.74	0.000152251	56198	Heyl	hairy/enhancer-of-split related with YRPW motif-like
1434809_at	-0.92	-0.57	-0.74	0.006480428	268970	Arhgap28	Rho GTPase activating protein 28
1450435_at	-0.62	-0.86	-0.74	2.39E-05	16728	L1cam	L1 cell adhesion molecule
1416168_at	-0.67	-0.82	-0.74	0.004675848	20317	Serpinf1	serine (or cysteine) peptidase inhibitor, clade F, member 1
1433643_at	-0.89	-0.60	-0.74	0.001445767	12293	Cacna2d1	calcium channel, voltage-dependent, alpha2/delta subunit 1
1439066_at	-0.79	-0.69	-0.74	4.03E-05	11600	Angpt1	angiopoietin 1
1449620_s_at	-0.77	-0.71	-0.74	2.31E-05	11515	Adcy9	adenylate cyclase 9
1456312_x_at	-0.76	-0.72	-0.74	5.86E-05	227753	Gsn	gelsolin
1456611_at	-0.60	-0.87	-0.74	0.013336385	58909	Fam13a	family with sequence similarity 13, member A
1421425_a_at	-0.69	-0.79	-0.74	4.90E-06	53901	Rcan2	regulator of calcineurin 2
1449823_at	-0.69	-0.78	-0.73	0.046835336	93837	Dach2	dachshund 2 (Drosophila)
1449383_at	-0.40	-1.07	-0.73	0.004886581	11565	Adssl1	adenylosuccinate synthetase like 1
1451475_at	-0.86	-0.60	-0.73	0.025655442	67784	Plxnd1	plexin D1
1418494_at	-0.07	-1.39	-0.73	0.012380726	13592	Ebf2	early B cell factor 2
1449871_at	-0.98	-0.48	-0.73	0.002749395	76365	Tbx18	T-box18
1428568_at	-0.95	-0.51	-0.73	0.000681243	68127	B230217C12Rik	RIKEN cDNA B230217C12 gene
1417577_at	-0.86	-0.60	-0.73	0.014409402	22065	Trpc3	transient receptor potential cation channel, subfamily C, member 3
1423049_a_at	-0.68	-0.77	-0.73	3.04E-05	22003	Tpm1	tropomyosin 1, alpha
1436195_at	-0.57	-0.88	-0.73	6.50E-05	192976	Fam211a	family with sequence similarity 211, member A
1418693_at	-0.77	-0.69	-0.73	1.15E-05	15381	Hnrnpc	heterogeneous nuclear ribonucleoprotein C
1455807_at	-0.76	-0.69	-0.72	5.11E-05	239364	Tspyl5	testis-specific protein, Y-encoded-like 5
1417633_at	-0.94	-0.51	-0.72	0.008086172	20657	Sod3	superoxide dismutase 3, extracellular
1431833_a_at	-0.75	-0.69	-0.72	0.033968078	15360	Hmgcs2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2
1448700_at	-1.14	-0.30	-0.72	0.008268759	14373	G0s2	G0/G1 switch gene 2
1424112_at	-0.30	-1.14	-0.72	0.046189508	16004	Igf2r	insulin-like growth factor 2 receptor
1423503_at	-0.76	-0.68	-0.72	6.34E-07	83964	Jam3	junction adhesion molecule 3

1426677_at	-0.71	-0.73	-0.72	1.64E-05	192176	Flna	filamin, alpha
1439794_at	-0.74	-0.69	-0.72	2.07E-06	57764	Ntn4	netrin 4
1430543_at	-0.66	-0.77	-0.72	0.003265791	76686	Clip3	CAP-GLY domain containing linker protein 3
1442018_at	-0.58	-0.85	-0.72	0.010449379	12226	Btg1	B cell translocation gene 1, anti-proliferative
1448421_s_at	-0.73	-0.70	-0.71	0.00021144	66695	Aspn	asporin
1456446_at	-0.73	-0.70	-0.71	0.026595192	67647	4930523C07Rik	RIKEN cDNA 4930523C07 gene
1423281_at	-0.81	-0.62	-0.71	0.001002874	20257	Stmn2	stathmin-like 2
1449799_s_at	-0.96	-0.46	-0.71	0.040037354	67451	Pkp2	plakophilin 2
1455970_at	-0.74	-0.69	-0.71	4.95E-05	242202	Pde5a	phosphodiesterase 5A, cGMP-specific
1438480_a_at	-0.71	-0.71	-0.71	0.001260296	77862	Thyn1	thymocyte nuclear protein 1
1420545_a_at	-0.56	-0.85	-0.71	0.002172752	108699	Chn1	chimerin (chimaerin) 1
1456401_at	-0.63	-0.78	-0.71	0.000405729	12296	Cacnb2	calcium channel, voltage-dependent, beta 2 subunit
1434194_at	-0.67	-0.74	-0.70	0.000338578	17756	Map2	microtubule-associated protein 2
1460197_a_at	-0.96	-0.45	-0.70	0.000769136	117167	Steap4	STEAP family member 4
1440397_at	-1.01	-0.39	-0.70	0.007621105	12293	Cacna2d1	calcium channel, voltage-dependent, alpha2/delta subunit 1
1450051_at	-0.47	-0.93	-0.70	0.00745255	22589	Atrx	alpha thalassemia/mental retardation syndrome X-linked homolog (human)
1417741_at	-0.33	-1.07	-0.70	0.011402284	110095	Pygl	liver glycogen phosphorylase
1423179_at	-0.68	-0.72	-0.70	0.000957846	16500	Kcnb1	potassium voltage gated channel, Shab-related subfamily, member 1
1429463_at	-0.89	-0.51	-0.70	0.020595053	108079	Prkaa2	protein kinase, AMP-activated, alpha 2 catalytic subunit
1448485_at	-0.93	-0.47	-0.70	0.009712417	14598	Ggt1	gamma-glutamyltransferase 1
1456397_at	-0.61	-0.79	-0.70	0.000201892	12561	Cdh4	cadherin 4
1449749_s_at	-0.76	-0.63	-0.70	0.002144695	224481	Tfb1m	transcription factor B1, mitochondrial
1427086_at	-0.75	-0.64	-0.70	0.000458151	20564	Slit3	slit homolog 3 (Drosophila)
1426892_at	-0.65	-0.74	-0.69	8.12E-05	22288	Utrn	utrophin
1443941_at	-0.70	-0.69	-0.69	1.61E-05	100503884	Ccdc149	coiled-coil domain containing 149
1436379_at	-0.62	-0.77	-0.69	2.36E-07	70461	Crtc3	CREB regulated transcription coactivator 3
1423141_at	-0.90	-0.49	-0.69	0.004330725	16889	Lipa	lysosomal acid lipase A
1421096_at	-0.71	-0.68	-0.69	0.000426889	22063	Trpc1	transient receptor potential cation channel, subfamily C, member 1
1418321_at	-0.84	-0.55	-0.69	8.66E-06	13177	Eci1	enoyl-Coenzyme A delta isomerase 1
1428801_at	-0.68	-0.71	-0.69	0.000187243	17309	Mgat3	mannoside acetylglucosaminyltransferase 3
1426733_at	-0.58	-0.80	-0.69	5.94E-06	217837	Itpk1	inositol 1,3,4-triphosphate 5/6 kinase
1436204_at	-0.82	-0.56	-0.69	3.43E-05	68786	1110059G02Rik	RIKEN cDNA 1110059G02 gene
1422642_at	-0.83	-0.55	-0.69	2.26E-05	260409	Cdc42ep3	CDC42 effector protein (Rho GTPase binding) 3
1435254_at	-0.75	-0.62	-0.68	6.13E-07	235611	Plxnb1	plexin B1
1450757_at	-0.93	-0.43	-0.68	0.001176504	12552	Cdh11	cadherin 11
1418595_at	-0.55	-0.81	-0.68	0.003365811	57435	Plin4	perilipin 4
1423500_a_at	-0.73	-0.63	-0.68	0.000532711	20678	Sox5	SRY-box containing gene 5
1456492_at	-0.42	-0.94	-0.68	0.000673247	74549	Mau2	MAU2 chromatid cohesion factor homolog (C. elegans)
1452114_s_at	-0.98	-0.38	-0.68	0.025781784	16011	Igfbp5	insulin-like growth factor binding protein 5
1419209_at	-0.93	-0.43	-0.68	0.013153828	14825	Cxcl1	chemokine (C-X-C motif) ligand 1
1422058_at	-0.69	-0.66	-0.68	0.000164929	18119	Nodal	nodal
1456197_x_at	-0.73	-0.62	-0.68	0.000509149	230959	Ajap1	adherens junction associated protein 1
1455336_at	-0.78	-0.57	-0.68	8.92E-05	66816	Thap2	THAP domain containing, apoptosis associated protein 2
1444564_at	-0.70	-0.65	-0.68	0.043166918	11815	Apod	apolipoprotein D
1455293_at	-0.75	-0.60	-0.68	0.007178004	235497	Leo1	Leo1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)
1418685_at	-0.73	-0.62	-0.68	0.000190031	117149	Tirap	toll-interleukin 1 receptor (TIR) domain-containing adaptor protein
1454014_a_at	-0.62	-0.73	-0.67	0.011915246	59030	Mkks	McKusick-Kaufman syndrome
1449527_at	-0.90	-0.45	-0.67	0.001467496	93878	Pcdhb7	protocadherin beta 7
1440346_at	-0.63	-0.72	-0.67	0.00565103	216850	Kdm6b	KDM1 lysine (K)-specific demethylase 6B
1415958_at	-0.68	-0.66	-0.67	0.000250042	20528	Slc2a4	solute carrier family 2 (facilitated glucose transporter), member 4
1437657_at	-0.50	-0.84	-0.67	0.001362524	244891	Scaper	S phase cyclin A-associated protein in the ER
1456658_at	-0.01	-1.32	-0.67	0.021328085	11475	Acta2	actin, alpha 2, smooth muscle, aorta
1452231_x_at	-0.87	-0.47	-0.67	0.005032146	100040462	Mndal	myeloid nuclear differentiation antigen like
1452231_x_at	-0.87	-0.47	-0.67	0.005032146	226695	Ifi205	interferon activated gene 205
1435082_at	-0.61	-0.72	-0.67	0.000315402	19027	Sypl	synaptophysin-like protein
1442061_at	-0.51	-0.83	-0.67	0.005122508	238386	Btbd7	BTB (POZ) domain containing 7
1423878_at	-0.78	-0.55	-0.66	4.60E-05	71683	Gypc	glycophorin C
1434051_s_at	-0.63	-0.70	-0.66	4.19E-05	73442	Hspa12a	heat shock protein 12A
1423858_a_at	-0.67	-0.65	-0.66	0.037277567	15360	Hmgcs2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2
1417832_at	-1.03	-0.30	-0.66	0.001253893	24061	Smc1a	structural maintenance of chromosomes 1A
1448602_at	-0.84	-0.48	-0.66	0.000263399	19309	Pygm	muscle glycogen phosphorylase
1418476_at	-0.72	-0.60	-0.66	0.000495128	12931	Crlf1	cytokine receptor-like factor 1
1416693_at	-0.41	-0.91	-0.66	0.000805264	14234	Foxc2	forkhead box C2
1433453_a_at	-0.65	-0.67	-0.66	0.000654304	99382	Abtb2	ankyrin repeat and BTB (POZ) domain containing 2
1460465_at	-0.79	-0.53	-0.66	0.004072655	68169	Ndnf	neuron-derived neurotrophic factor
1433184_at	-0.47	-0.85	-0.66	0.00760321	77731	6720477C19Rik	RIKEN cDNA 6720477C19 gene
1428861_at	-0.61	-0.71	-0.66	2.00E-07	78749	Filip1l	filamin A interacting protein 1-like
1421818_at	-0.62	-0.70	-0.66	1.04E-05	12053	Bcl6	B cell leukemia/lymphoma 6
1427267_at	-0.78	-0.53	-0.66	0.000700056	231861	Tnrc18	trinucleotide repeat containing 18
1440252_at	-0.66	-0.65	-0.65	0.00251221	232440	H2afj	H2A histone family, member J
1425811_a_at	-0.86	-0.45	-0.65	0.001630839	13007	Csrp1	cysteine and glycine-rich protein 1
1452876_x_at	-0.78	-0.53	-0.65	0.000419275	72139	2610044O15Rik8	RIKEN cDNA 2610044O15 gene
1435265_at	-0.59	-0.71	-0.65	1.39E-06	67731	Fbxo32	F-box protein 32
1452363_a_at	-0.59	-0.72	-0.65	4.46E-07	11938	Atp2a2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
1441206_at	-0.66	-0.65	-0.65	0.001163277	118449	Synpo2	synaptopodin 2
1448856_a_at	-0.63	-0.67	-0.65	3.43E-06	110265	Msra	methionine sulfoxide reductase A
1424768_at	-0.50	-0.80	-0.65	9.96E-05	109624	Cald1	caldesmon 1

1454803_a_at	-0.59	-0.71	-0.65	0.000205431	232232	Hdac11	histone deacetylase 11
1449298_a_at	-0.43	-0.87	-0.65	0.000141901	18573	Pde1a	phosphodiesterase 1A, calmodulin-dependent
1417022_at	-0.77	-0.53	-0.65	0.042741285	11989	Slc7a3	solute carrier family 7 (cationic amino acid transporter, y+ system), member 3
1456885_at	-0.53	-0.77	-0.65	1.98E-05	20362	08-Sep	septin 8
1421504_at	-0.65	-0.65	-0.65	0.000102939	20688	Sp4	trans-acting transcription factor 4
1434045_at	-0.59	-0.71	-0.65	0.000277601	12576	Cdkn1b	cyclin-dependent kinase inhibitor 1B
1453145_at	-0.56	-0.73	-0.65	0.000439278	66776	Pisd-ps3	phosphatidylserine decarboxylase, pseudogene 3
1427942_at	-0.79	-0.50	-0.64	0.00132409	237504	Rassf9	Ras association (RalGDS/AF-6) domain family (N-terminal) member 9
1423104_at	-0.65	-0.64	-0.64	0.000273303	16367	Irs1	insulin receptor substrate 1
1455836_at	-0.45	-0.84	-0.64	0.007672541	18789	Papola	poly (A) polymerase alpha
1422731_at	-0.74	-0.55	-0.64	1.58E-06	29806	Limd1	LIM domains containing 1
1429196_at	-0.59	-0.69	-0.64	0.004915465	29809	Rabgap1l	RAB GTPase activating protein 1-like
1418711_at	-0.69	-0.59	-0.64	2.74E-07	18590	Pdgfa	platelet derived growth factor, alpha
1452620_at	-0.67	-0.61	-0.64	1.97E-05	74551	Pck2	phosphoenolpyruvate carboxykinase 2 (mitochondrial)
1448728_a_at	-0.80	-0.48	-0.64	0.039099309	80859	Nfkbiz	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, zeta
1426995_a_at	-0.71	-0.57	-0.64	0.000164725	11692	Gfer	growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)
1428808_at	-0.67	-0.61	-0.64	3.03E-05	243548	Prickle2	prickle homolog 2 (Drosophila)
1427371_at	-0.60	-0.68	-0.64	0.003738832	217258	Abca8a	ATP-binding cassette, sub-family A (ABC1), member 8a
1451990_at	-0.65	-0.63	-0.64	1.52E-08	212307	Mapre2	microtubule-associated protein, RP/EB family, member 2
1417011_at	-0.72	-0.55	-0.64	2.73E-05	15529	Sdc2	syndecan 2
1455150_at	-0.90	-0.38	-0.64	0.008979003	329152	Hecw2	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2
1429150_at	-0.76	-0.51	-0.63	0.007055982	67200	Ccdc77	coiled-coil domain containing 77
1427201_at	-0.55	-0.72	-0.63	0.000457546	66175	Mustn1	musculoskeletal, embryonic nuclear protein 1
1452840_at	-0.67	-0.60	-0.63	0.000240394	69784	1500009L16Rik	RIKEN cDNA 1500009L16 gene
1424897_at	-0.91	-0.36	-0.63	0.005790934	64450	Gpr85	G protein-coupled receptor 85
1440132_s_at	-0.80	-0.46	-0.63	6.72E-05	19085	Prkar1b	protein kinase, cAMP dependent regulatory, type I beta
1422510_at	-0.53	-0.73	-0.63	1.18E-05	69274	Ctdspl	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like
1435160_at	-0.55	-0.71	-0.63	0.011059947	268390	Ahsa2	AHA1, activator of heat shock protein ATPase 2
1434441_at	-0.62	-0.64	-0.63	0.005334421	66129	Aaed1	AhpC/TSA antioxidant enzyme domain containing 1
1448227_at	-0.77	-0.49	-0.63	0.021765926	14786	Grb7	growth factor receptor bound protein 7
1451969_s_at	-0.65	-0.61	-0.63	0.000522218	235587	Parp3	poly (ADP-ribose) polymerase family, member 3
1458439_a_at	-0.61	-0.64	-0.63	0.000979387	224170	Dzip3	DAZ interacting protein 3, zinc finger
1420429_at	-0.74	-0.52	-0.63	4.32E-05	93874	Pcdhb3	protocadherin beta 3
1455956_x_at	-0.69	-0.56	-0.63	2.18E-05	12444	Ccnd2	cyclin D2
1456225_x_at	-0.79	-0.46	-0.63	0.04932477	228775	Trib3	tribbles homolog 3 (Drosophila)
1451431_a_at	-0.67	-0.59	-0.63	0.000488745	52840	Dbndd2	dysbindin (dystrobrevin binding protein 1) domain containing 2
1429389_at	-0.79	-0.46	-0.63	0.002855713	74729	Setmar	SET domain without mariner transposase fusion
1438115_a_at	-0.67	-0.59	-0.63	7.45E-05	26941	Slc9a3r1	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1
1426801_at	-0.62	-0.63	-0.63	2.02E-06	20362	08-Sep	septin 8
1427011_a_at	-0.70	-0.55	-0.63	3.68E-07	14768	Lancl1	LanC (bacterial lantibiotic synthetase component C)-like 1
1454838_s_at	-0.71	-0.54	-0.62	0.002372266	106522	Pkdcc	protein kinase domain containing, cytoplasmic
1436894_at	-0.54	-0.71	-0.62	0.000131749	100039795	Ildr2	immunoglobulin-like domain containing receptor 2
1439073_at	-0.71	-0.54	-0.62	8.41E-05	224585	Zfp160	zinc finger protein 160
1436830_at	-0.48	-0.77	-0.62	0.00521029	277010	Marveld1	MARVEL (membrane-associating) domain containing 1
1426565_at	-0.67	-0.57	-0.62	0.012646622	16001	Igf1r	insulin-like growth factor I receptor
1417704_a_at	-0.56	-0.68	-0.62	0.00203902	11856	Arhgap6	Rho GTPase activating protein 6
1442791_x_at	-0.48	-0.77	-0.62	0.005794486	77890	6720407P12Rik	RIKEN cDNA 6720407P12 gene
1439618_at	-0.86	-0.38	-0.62	0.001163613	23984	Pde10a	phosphodiesterase 10A
1440770_at	-0.53	-0.71	-0.62	0.020986347	12043	Bcl2	B cell leukemia/lymphoma 2
1437734_at	-0.59	-0.66	-0.62	1.66E-05	17931	Ppp1r12a	protein phosphatase 1, regulatory (inhibitor) subunit 12A
1460729_at	-0.59	-0.65	-0.62	4.06E-05	19877	Rock1	Rho-associated coiled-coil containing protein kinase 1
1416286_at	-0.66	-0.58	-0.62	2.91E-06	19736	Rgs4	regulator of G-protein signaling 4
1416935_at	-0.44	-0.80	-0.62	2.91E-05	22368	Trpv2	transient receptor potential cation channel, subfamily V, member 2
1457744_at	-0.54	-0.70	-0.62	0.009462817	212880	Ddx46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46
1453435_a_at	-0.68	-0.56	-0.62	0.04256971	55990	Fmo2	flavin containing monooxygenase 2
1448502_at	-0.10	-1.13	-0.62	0.016891525	20503	Slc16a7	solute carrier family 16 (monocarboxylic acid transporters), member 7
1418789_at	-0.69	-0.55	-0.62	0.025127965	268534	Sntg2	syntrophin, gamma 2
1440147_at	-0.37	-0.86	-0.62	0.01165544	246316	Lgl2	leucine-rich repeat LGI family, member 2
1449292_at	-0.49	-0.74	-0.62	0.002092415	12421	Rb1cc1	RB1-inducible coiled-coil 1
1448545_at	-0.71	-0.52	-0.62	4.75E-05	15529	Sdc2	syndecan 2
1437497_a_at	-0.60	-0.63	-0.62	0.000237588	15519	Hsp90aa1	heat shock protein 90, alpha (cytosolic), class A member 1
1448229_s_at	-0.56	-0.67	-0.61	2.63E-06	12444	Ccnd2	cyclin D2
1442180_at	-0.76	-0.47	-0.61	0.037992859	239133	Dleu7	deleted in lymphocytic leukemia, 7
1449533_at	-0.59	-0.64	-0.61	0.021667771	67888	Tmem100	transmembrane protein 100
1450716_at	-0.64	-0.58	-0.61	0.010022105	11504	Adamts1	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 1
1436505_at	-0.66	-0.57	-0.61	9.26E-05	228005	Ppig	peptidyl-prolyl isomerase G (cyclophilin G)
1444229_at	-0.43	-0.80	-0.61	0.013702059	11819	Nr2f2	nuclear receptor subfamily 2, group F, member 2
1423274_at	-0.71	-0.51	-0.61	0.000226048	18130	Ints6	integrator complex subunit 6
1417235_at	-0.73	-0.49	-0.61	2.76E-06	57440	Ehd3	EH-domain containing 3
1416551_at	-0.56	-0.66	-0.61	3.63E-09	11938	Atp2a2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
1418511_at	0.00	-1.22	-0.61	0.015572477	56429	Dpt	dermatopontin
1440227_at	-0.48	-0.74	-0.61	0.032109701	53881	Slc5a3	solute carrier family 5 (inositol transporters), member 3
1423586_at	-0.59	-0.63	-0.61	1.17E-06	26362	Axl	AXL receptor tyrosine kinase
1456656_at	-0.54	-0.67	-0.61	0.049073094	108030	Lin7a	lin-7 homolog A (C. elegans)
1419697_at	-0.71	-0.51	-0.61	2.60E-05	56066	Cxcl11	chemokine (C-X-C motif) ligand 11
1438796_at	-0.86	-0.35	-0.61	0.042023448	18124	Nr4a3	nuclear receptor subfamily 4, group A, member 3
1428730_at	-0.41	-0.80	-0.61	0.027052754	79264	Krit1	KRIT1, ankyrin repeat containing

1444524_at	-0.73	-0.48	-0.61	2.32E-05	100043424	Gm14005	predicted gene 14005
1431176_at	-0.17	-1.04	-0.61	0.011924534	66371	Chmp4c	charged multivesicular body protein 4C
1424450_at	-0.33	-0.88	-0.61	0.018006338	70355	Gprc5c	G protein-coupled receptor, family C, group 5, member C
1417307_at	-0.67	-0.54	-0.61	5.51E-05	13405	Dmd	dystrophin, muscular dystrophy
1433742_at	-0.58	-0.63	-0.60	0.00026513	107351	Kank1	KN motif and ankyrin repeat domains 1
1434442_at	-0.66	-0.54	-0.60	0.014592301	52331	Stbd1	starch binding domain 1
1417736_at	-0.53	-0.68	-0.60	0.002585041	67241	Smc6	structural maintenance of chromosomes 6
1456483_at	-0.64	-0.56	-0.60	0.00068975	22750	Zfp9	zinc finger protein 9
1429506_at	-0.74	-0.46	-0.60	0.001020102	93960	Nkd1	naked cuticle 1 homolog (Drosophila)
1438702_at	-0.50	-0.70	-0.60	0.002285116	399558	Flrt2	fibronectin leucine rich transmembrane protein 2
1440801_s_at	-0.50	-0.71	-0.60	0.00010006	320129	Adrbk2	adrenergic receptor kinase, beta 2
1417219_s_at	-1.08	-0.12	-0.60	0.023319908	19240	Tmsb10	thymosin, beta 10
1438726_at	-0.85	-0.34	-0.60	0.019529199	320878	Mical2	microtubule associated monoxygenase, calponin and LIM domain containing 2
1430127_a_at	-0.66	-0.54	-0.60	0.000656402	12444	Ccnd2	cyclin D2
1416995_at	-0.32	-0.88	-0.60	0.011827632	80708	Pacsin3	protein kinase C and casein kinase substrate in neurons 3
1437222_x_at	-0.48	-0.72	-0.60	0.000186599	382985	Rrm2b	ribonucleotide reductase M2 B (TP53 inducible)
1437784_at	-0.39	-0.81	-0.60	0.001187559	12395	Runx1t1	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)
1429129_at	-0.70	-0.49	-0.60	0.001583015	71710	Lrrcc1	leucine rich repeat and coiled-coil domain containing 1
1452020_a_at	-0.65	-0.54	-0.59	4.29E-06	30954	Siva1	SIVA1, apoptosis-inducing factor
1452879_at	-0.69	-0.50	-0.59	0.027490561	118449	Synpo2	synaptopodin 2
1450982_at	-0.67	-0.52	-0.59	0.00024515	26941	Slc9a3r1	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1
1425339_at	-0.64	-0.55	-0.59	0.000950682	18798	Plcb4	phospholipase C, beta 4
1451778_at	-0.82	-0.37	-0.59	0.022265317	70461	Crtc3	CREB regulated transcription coactivator 3
1429444_at	-0.31	-0.87	-0.59	0.007751005	68895	Rasl11a	RAS-like, family 11, member A
1434647_at	-0.61	-0.57	-0.59	0.00043634	268780	Egflam	EGF-like, fibronectin type III and laminin G domains
1439757_s_at	-0.63	-0.56	-0.59	9.81E-07	13838	Epha4	Eph receptor A4
1418122_at	-0.40	-0.79	-0.59	0.00162143	17880	Myh11	myosin, heavy polypeptide 11, smooth muscle
1459838_s_at	-0.71	-0.47	-0.59	0.025258692	74007	Btbd11	BTB (POZ) domain containing 11
1434745_at	-0.60	-0.58	-0.59	5.00E-07	12444	Ccnd2	cyclin D2
1424504_at	-0.55	-0.63	-0.59	0.000357845	19334	Rab22a	RAB22A, member RAS oncogene family
1416158_at	-0.64	-0.54	-0.59	0.001101022	11819	Nr2f2	nuclear receptor subfamily 2, group F, member 2
1438082_at	-0.51	-0.67	-0.59	0.000128865	66950	Tmem206	transmembrane protein 206
1424770_at	-0.56	-0.62	-0.59	8.39E-06	109624	Cald1	caldesmon 1
1428899_at	-0.59	-0.59	-0.59	0.000656601	381339	Tmem182	transmembrane protein 182
1422640_at	-0.72	-0.46	-0.59	0.000875651	93880	Pcdhb9	protocadherin beta 9
1452848_at	-0.54	-0.63	-0.59	2.23E-05	77106	Tmem181a	transmembrane protein 181A
1452848_at	-0.54	-0.63	-0.59	2.23E-05	547127	Tmem181b-ps	transmembrane protein 181B, pseudogene
1447914_x_at	-0.65	-0.52	-0.59	0.017490947	72446	Prr5l	proline rich 5 like
1424338_at	-0.77	-0.41	-0.59	0.003654907	14412	Slc6a13	solute carrier family 6 (neurotransmitter transporter, GABA), member 13
1429487_at	-0.56	-0.61	-0.59	3.25E-05	17931	Ppp1r12a	protein phosphatase 1, regulatory (inhibitor) subunit 12A
1425506_at	-0.53	-0.64	-0.59	2.66E-05	107589	Mylk	myosin, light polypeptide kinase
1456791_at	-0.74	-0.43	-0.58	0.022838888	627049	Zfp800	zinc finger protein 800
1429897_a_at	-0.70	-0.47	-0.58	0.033519395	67102	D16Ertd472e	DNA segment, Chr 16, ERATO Doi 472, expressed
1451322_at	-0.55	-0.62	-0.58	0.000328963	69574	Cmbl	carboxymethylenebutenolidase-like (Pseudomonas)
1426360_at	-0.56	-0.60	-0.58	0.000626367	70579	Zc3h11a	zinc finger CCCH type containing 11A
1426360_at	-0.56	-0.60	-0.58	0.000626367	667118	Zbed6	zinc finger, BED domain containing 6
1430568_at	-0.57	-0.60	-0.58	0.000334342	67302	Zc3h13	zinc finger CCCH type containing 13
1436332_at	-0.49	-0.68	-0.58	0.017417638	243912	Hspb6	heat shock protein, alpha-crystallin-related, B6
1416713_at	-0.62	-0.54	-0.58	3.23E-05	67971	Tppp3	tubulin polymerization-promoting protein family member 3
1425826_a_at	-0.61	-0.56	-0.58	3.37E-05	20411	Sorbs1	sorbin and SH3 domain containing 1
1447100_s_at	-0.62	-0.54	-0.58	1.01E-06	70617	5730508B09Rik	RIKEN cDNA 5730508B09 gene
1416549_at	-0.45	-0.71	-0.58	0.000464343	58246	Slc35b4	solute carrier family 35, member B4
1427465_at	-0.71	-0.45	-0.58	8.65E-05	98660	Atp1a2	ATPase, Na+/K+ transporting, alpha 2 polypeptide
1424567_at	-0.63	-0.53	-0.58	0.001911089	70747	Tspan2	tetraspanin 2
1442143_at	-0.15	-1.01	-0.58	0.035152848	320091	Ano4	anoctamin 4
1452373_at	-0.50	-0.66	-0.58	0.000692652	76719	Kansl1	KAT8 regulatory NSL complex subunit 1
1450700_at	-0.66	-0.50	-0.58	1.26E-06	260409	Cdc42ep3	CDC42 effector protein (Rho GTPase binding) 3
1425156_at	-0.48	-0.68	-0.58	0.007305022	229900	Gbp7	guanylate binding protein 7
1426210_x_at	-0.60	-0.56	-0.58	0.000300927	235587	Parp3	poly (ADP-ribose) polymerase family, member 3
1420622_a_at	-0.57	-0.58	-0.58	0.014555762	15481	Hspa8	heat shock protein 8
1454848_at	-0.53	-0.62	-0.58	0.000202005	232807	Ppp1r12c	protein phosphatase 1, regulatory (inhibitor) subunit 12C
1426914_at	-0.55	-0.60	-0.58	0.013230918	218518	Marveld2	MARVEL (membrane-associating) domain containing 2
1448665_at	-0.61	-0.54	-0.58	0.000184938	13405	Dmd	dystrophin, muscular dystrophy
1426906_at	-0.81	-0.34	-0.57	0.006521065	226695	Ifi205	interferon activated gene 205
1426906_at	-0.81	-0.34	-0.57	0.006521065	100040462	Mndal	myeloid nuclear differentiation antigen like
1451642_at	-0.61	-0.54	-0.57	0.000789608	16561	Kif1b	kinesin family member 1B
1432189_a_at	-0.32	-0.83	-0.57	0.009743611	20678	Sox5	SRY-box containing gene 5
1444060_at	-0.50	-0.65	-0.57	0.004858944	69909	2610027K06Rik	RIKEN cDNA 2610027K06 gene
1435459_at	-0.69	-0.46	-0.57	0.046150248	55990	Fmo2	flavin containing monooxygenase 2
1423941_at	-0.65	-0.49	-0.57	6.44E-05	12325	Camk2g	calcium/calmodulin-dependent protein kinase II gamma
1434766_at	-0.71	-0.43	-0.57	0.007871846	108079	Prkaa2	protein kinase, AMP-activated, alpha 2 catalytic subunit
1435148_at	-0.73	-0.42	-0.57	7.97E-05	11932	Atp1b2	ATPase, Na+/K+ transporting, beta 2 polypeptide
1448894_at	-0.86	-0.28	-0.57	0.001345664	14187	Akr1b8	aldo-keto reductase family 1, member B8
1452761_a_at	-0.64	-0.50	-0.57	0.000202046	207181	Rbms3	RNA binding motif, single stranded interacting protein
1435029_at	-0.48	-0.66	-0.57	3.47E-05	65964	B230120H23Rik	RIKEN cDNA B230120H23 gene
1419508_at	-0.48	-0.66	-0.57	0.022187217	19766	Ripk1	receptor (TNFRSF)-interacting serine-threonine kinase 1
1440761_at	-0.30	-0.84	-0.57	0.001623147	373852	4833422C13Rik	RIKEN cDNA 4833422C13 gene

1440838_at	-0.41	-0.73	-0.57	0.004650911	16500	Kcnb1	potassium voltage gated channel, Shab-related subfamily, member 1
1437884_at	-0.62	-0.52	-0.57	0.01037498	75869	Arl5b	ADP-ribosylation factor-like 5B
1419811_at	-0.59	-0.55	-0.57	7.84E-06	11515	Adcy9	adenylate cyclase 9
1453465_x_at	-0.84	-0.29	-0.57	0.014200034	100043766	Gm14057	Ppp1r14c pseudogene
1435663_at	-0.26	-0.88	-0.57	0.031567462	13982	Esr1	estrogen receptor 1 (alpha)
1429678_at	-0.54	-0.59	-0.57	5.16E-06	70617	5730508B09Rik	RIKEN cDNA 5730508B09 gene
1425102_a_at	-0.83	-0.30	-0.57	0.001486684	70008	Ace2	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2
1419070_at	-0.85	-0.28	-0.56	0.014196897	12879	Cys1	cystin 1
1420942_s_at	-0.46	-0.67	-0.56	0.000286771	19737	Rgs5	regulator of G-protein signaling 5
1451567_a_at	-0.69	-0.44	-0.56	0.026128023	100504287	Gm16340	predicted gene 16340
1451567_a_at	-0.69	-0.44	-0.56	0.026128023	100862473	LOC100862473	uncharacterized LOC100862473
1451567_a_at	-0.69	-0.44	-0.56	0.026128023	15950	Ifi203	interferon activated gene 203
1425750_a_at	-0.43	-0.70	-0.56	0.003776672	16453	Jak3	Janus kinase 3
1430220_at	-0.42	-0.71	-0.56	0.000516502	67392	4833420G17Rik	RIKEN cDNA 4833420G17 gene
1437057_at	-0.67	-0.45	-0.56	0.003606466	230971	Megf6	multiple EGF-like-domains 6
1431811_a_at	-0.41	-0.72	-0.56	0.019124365	78938	Fbxo34	F-box protein 34
1422912_at	-0.42	-0.70	-0.56	0.001543467	12159	Bmp4	bone morphogenetic protein 4
1447685_x_at	-0.52	-0.60	-0.56	0.00551794	23872	Ets2	E26 avian leukemia oncogene 2, 3' domain
1420661_a_at	-0.72	-0.40	-0.56	0.001102533	66771	Gid4	GID complex subunit 4, VID24 homolog (S. cerevisiae)
1437636_at	-0.72	-0.39	-0.56	0.013423438	623121	Pydc4	pyrin domain containing 4
1430539_at	-0.69	-0.43	-0.56	3.53E-05	67622	Mxra7	matrix-remodelling associated 7
1458385_at	-0.44	-0.67	-0.56	0.01046257	18415	Hspa4l	heat shock protein 4 like
1419639_at	-0.59	-0.52	-0.56	0.001258957	13642	Efnb2	ephrin B2
1432419_a_at	-0.53	-0.58	-0.56	0.000247743	101513	Mob2	MOB kinase activator 2
1452923_at	-0.60	-0.51	-0.56	0.000102664	75597	Ndufaf2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 2
1426244_at	-0.45	-0.66	-0.56	4.95E-06	212307	Mapre2	microtubule-associated protein, RP/EB family, member 2
1428750_at	-0.93	-0.18	-0.55	0.015125149	104252	Cdc42ep2	CDC42 effector protein (Rho GTPase binding) 2
1451029_at	-0.40	-0.70	-0.55	0.010344159	12050	Bcl2l2	BCL2-like 2
1449519_at	-0.60	-0.50	-0.55	0.004294143	13197	Gadd45a	growth arrest and DNA-damage-inducible 45 alpha
1438680_at	-0.65	-0.45	-0.55	0.000900202	319974	Auts2	autism susceptibility candidate 2
1452138_a_at	-0.66	-0.45	-0.55	5.94E-05	70008	Ace2	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2
1452070_at	-0.63	-0.48	-0.55	0.031948463	67379	Dedd2	death effector domain-containing DNA binding protein 2
1434073_at	-0.68	-0.42	-0.55	0.002094947	245607	Gprasp2	G protein-coupled receptor associated sorting protein 2
1451731_at	-0.61	-0.49	-0.55	5.60E-06	27410	Abca3	ATP-binding cassette, sub-family A (ABC1), member 3
1447612_x_at	-0.46	-0.64	-0.55	0.009849385	216850	Kdm6b	KDM1 lysine (K)-specific demethylase 6B
1441295_at	-0.48	-0.62	-0.55	0.010156604	214895	Lman2l	lectin, mannose-binding 2-like
1456685_at	-0.20	-0.90	-0.55	0.009754669	18197	Nsg2	neuron specific gene family member 2
1422805_a_at	-0.66	-0.43	-0.55	0.001961921	71777	Ing3	inhibitor of growth family, member 3
1423201_at	-0.51	-0.59	-0.55	0.000693936	20185	Ncor1	nuclear receptor co-repressor 1
1416160_at	-0.42	-0.67	-0.55	0.016803515	11819	Nr2f2	nuclear receptor subfamily 2, group F, member 2
1439627_at	-0.59	-0.50	-0.55	0.000758294	22771	Zic1	zinc finger protein of the cerebellum 1
1460314_s_at	-0.36	-0.73	-0.54	0.001912363	319149	Hist1h3d	histone cluster 1, H3d
1460314_s_at	-0.36	-0.73	-0.54	0.001912363	260423	Hist1h3f	histone cluster 1, H3f
1460314_s_at	-0.36	-0.73	-0.54	0.001912363	97114	Hist2h3c2	histone cluster 2, H3c2
1460314_s_at	-0.36	-0.73	-0.54	0.001912363	319150	Hist1h3b	histone cluster 1, H3b
1460314_s_at	-0.36	-0.73	-0.54	0.001912363	319151	Hist1h3e	histone cluster 1, H3e
1460314_s_at	-0.36	-0.73	-0.54	0.001912363	319148	Hist1h3c	histone cluster 1, H3c
1460314_s_at	-0.36	-0.73	-0.54	0.001912363	15077	Hist2h3c1	histone cluster 2, H3c1
1460314_s_at	-0.36	-0.73	-0.54	0.001912363	319154	Hist2h3b	histone cluster 2, H3b
1460314_s_at	-0.36	-0.73	-0.54	0.001912363	360198	Hist1h3a	histone cluster 1, H3a
1460314_s_at	-0.36	-0.73	-0.54	0.001912363	319152	Hist1h3h	histone cluster 1, H3h
1460314_s_at	-0.36	-0.73	-0.54	0.001912363	319153	Hist1h3i	histone cluster 1, H3i
1460314_s_at	-0.36	-0.73	-0.54	0.001912363	97908	Hist1h3g	histone cluster 1, H3g
1449187_at	-0.49	-0.59	-0.54	0.000162987	18590	Pdgfa	platelet derived growth factor, alpha
1422701_at	-0.66	-0.43	-0.54	0.041533119	22637	Zap70	zeta-chain (TCR) associated protein kinase
1421163_a_at	-0.47	-0.61	-0.54	0.003972016	18027	Nfia	nuclear factor I/A
1437217_at	-0.63	-0.46	-0.54	0.004941551	140577	Ankrd6	ankyrin repeat domain 6
1422340_a_at	-0.59	-0.50	-0.54	0.013859349	11468	Actg2	actin, gamma 2, smooth muscle, enteric
1440970_at	-0.23	-0.86	-0.54	0.017692553	545156	Kalrn	kalirin, RhoGEF kinase
1429363_at	-0.59	-0.49	-0.54	0.000110009	52348	Vps37a	vacuolar protein sorting 37A (yeast)
1420946_at	-0.77	-0.31	-0.54	0.004237276	22589	Atrx	alpha thalassemia/mental retardation syndrome X-linked homolog (human)
1428799_at	-0.62	-0.46	-0.54	0.001745415	75782	Lca5	Leber congenital amaurosis 5 (human)
1437221_at	-0.42	-0.66	-0.54	0.000313732	382985	Rrm2b	ribonucleotide reductase M2 B (TP53 inducible)
1421064_at	-0.49	-0.59	-0.54	1.29E-05	56217	Mpp5	membrane protein, palmitoylated 5 (MAGUK p55 subfamily member 5)
1452180_at	-0.45	-0.62	-0.54	0.009243006	269424	Phf17	PHD finger protein 17
1419985_s_at	-0.61	-0.47	-0.54	0.000137965	52570	Ccdc69	coiled-coil domain containing 69
1418586_at	-0.47	-0.61	-0.54	5.42E-06	11515	Adcy9	adenylate cyclase 9
1457434_s_at	-0.62	-0.46	-0.54	0.000149897	30963	Ptpla	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a
1457644_s_at	-0.79	-0.29	-0.54	0.03190998	14825	Cxcl1	chemokine (C-X-C motif) ligand 1
1449048_s_at	-0.67	-0.40	-0.54	0.001044321	19341	Rab4a	RAB4A, member RAS oncogene family
1452940_x_at	-0.43	-0.65	-0.54	0.001958033	71795	Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1
1460645_at	-0.47	-0.60	-0.53	0.008158569	66917	Chordc1	cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1
1458892_at	-0.10	-0.97	-0.53	0.020141347	102344	9430047G12Rik	RIKEN cDNA 9430047G12 gene
1436239_at	-0.71	-0.36	-0.53	0.040809866	114479	Slc5a5	solute carrier family 5 (sodium iodide symporter), member 5
1417439_at	-0.65	-0.42	-0.53	0.000167586	70445	Cd248	CD248 antigen, endosialin
1457342_at	-0.46	-0.61	-0.53	0.000580741	22781	Ikzf4	IKAROS family zinc finger 4
1420940_x_at	-0.48	-0.59	-0.53	1.68E-05	19737	Rgs5	regulator of G-protein signaling 5

1457751_at	-0.48	-0.58	-0.53	0.003295228	233532	Rsf1	remodeling and spacing factor 1
1426651_at	-0.60	-0.47	-0.53	0.000126136	69163	Mrpl44	mitochondrial ribosomal protein L44
1425528_at	-0.64	-0.42	-0.53	0.001199061	18933	Prrx1	paired related homeobox 1
1455238_at	-0.88	-0.18	-0.53	0.036114495	245631	Mum1l1	melanoma associated antigen (mutated) 1-like 1
1422748_at	-0.40	-0.65	-0.53	0.000358316	24136	Zeb2	zinc finger E-box binding homeobox 2
1449303_at	-0.47	-0.59	-0.53	0.000236773	75747	Sesn3	sestrin 3
1437403_at	-0.28	-0.78	-0.53	0.007832377	320825	Samd5	sterile alpha motif domain containing 5
1458470_at	-0.28	-0.78	-0.53	0.02807245	320174	A830082K12Rik	RIKEN cDNA A830082K12 gene
1444058_at	-0.38	-0.67	-0.52	0.006152037	224170	Dzip3	DAZ interacting protein 3, zinc finger
1449262_s_at	-0.36	-0.68	-0.52	0.009781494	22343	Lin7c	lin-7 homolog C (C. elegans)
1429452_x_at	-0.59	-0.45	-0.52	0.0019257	66776	Pisd-ps3	phosphatidylserine decarboxylase, pseudogene 3
1448469_at	-0.70	-0.35	-0.52	0.01179076	18073	Nid1	nidogen 1
1434755_at	-0.63	-0.41	-0.52	0.026255929	235431	Coro2b	coronin, actin binding protein, 2B
1418514_at	-0.60	-0.44	-0.52	0.029499432	17765	Mtf2	metal response element binding transcription factor 2
1452316_at	-0.41	-0.63	-0.52	0.002071763	71793	Ints12	integrator complex subunit 12
1438164_x_at	-0.46	-0.58	-0.52	1.61E-05	14252	Flot2	flotillin 2
1416625_at	-0.72	-0.32	-0.52	0.00033911	12258	Serping1	serine (or cysteine) peptidase inhibitor, clade G, member 1
1435743_at	-0.43	-0.61	-0.52	0.000518607	277396	Klhl23	kelch-like 23
1453750_x_at	-0.32	-0.72	-0.52	0.003680545	71795	Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1
1444232_at	-0.58	-0.45	-0.52	0.000442145	19091	Prkg1	protein kinase, cGMP-dependent, type I
1417821_at	-0.34	-0.69	-0.52	0.008532119	110956	D17H6S56E-5	DNA segment, Chr 17, human D6S56E 5
1425031_at	-0.41	-0.62	-0.51	0.029679474	246179	Fktn	fukutin
1450464_at	-0.42	-0.61	-0.51	0.000161673	13560	E4f1	E4F transcription factor 1
1452722_a_at	-0.32	-0.71	-0.51	0.019823059	75717	Cul5	cullin 5
1435901_at	-0.40	-0.63	-0.51	0.002559348	227334	Usp40	ubiquitin specific peptidase 40
1425891_a_at	-0.71	-0.32	-0.51	0.000400968	66790	Grtp1	GH regulated TBC protein 1
1436172_at	-0.60	-0.43	-0.51	4.82E-05	330256	Gm20559	predicted gene, 20559
1451474_a_at	-0.27	-0.76	-0.51	0.002170198	52552	Parp8	poly (ADP-ribose) polymerase family, member 8
1422064_a_at	-0.66	-0.37	-0.51	0.001537755	56490	Zbtb20	zinc finger and BTB domain containing 20
1425493_at	-0.41	-0.61	-0.51	0.000233842	12166	Bmpr1a	bone morphogenetic protein receptor, type 1A
1418524_at	-0.75	-0.27	-0.51	0.009212684	18536	Pcm1	pericentriolar material 1
1417636_at	-0.84	-0.18	-0.51	0.023208124	14664	Slc6a9	solute carrier family 6 (neurotransmitter transporter, glycine), member 9
1436125_at	-0.42	-0.60	-0.51	0.007722865	67102	D16Ertd472e	DNA segment, Chr 16, ERATO Doi 472, expressed
1429390_at	-0.31	-0.71	-0.51	0.001308017	235534	Acpl2	acid phosphatase-like 2
1452385_at	-0.58	-0.43	-0.51	1.96E-05	99526	Usp53	ubiquitin specific peptidase 53
1448411_at	-0.59	-0.43	-0.51	2.27E-05	22393	Wfs1	Wolfram syndrome 1 homolog (human)
1436560_at	-0.42	-0.59	-0.51	0.001245485	16568	Kif3a	kinesin family member 3A
1415859_at	-0.60	-0.42	-0.51	0.000187477	56347	Eif3c	eukaryotic translation initiation factor 3, subunit C
1460006_at	-0.25	-0.77	-0.51	0.021842589	11906	Zfhx3	zinc finger homeobox 3
1423065_at	-0.36	-0.65	-0.50	0.019643446	13435	Dnmt3a	DNA methyltransferase 3A
1435910_at	-0.59	-0.41	-0.50	0.000302699	60527	Fads3	fatty acid desaturase 3
1417626_at	-0.78	-0.22	-0.50	0.028662446	83679	Pde4dip	phosphodiesterase 4D interacting protein (myomegalin)
1458534_at	-0.64	-0.36	-0.50	0.003459587	52882	Rgs7bp	regulator of G-protein signalling 7 binding protein
1420650_at	-0.28	-0.72	-0.50	0.004630335	11906	Zfhx3	zinc finger homeobox 3
1440381_at	-0.60	-0.39	-0.50	0.004443987	67045	Riok2	RIO kinase 2 (yeast)
1422231_a_at	-0.77	-0.23	-0.50	0.046206673	85030	Tnfrsf25	tumor necrosis factor receptor superfamily, member 25
1450178_at	-0.69	-0.30	-0.50	0.005646331	114642	Brdt	bromodomain, testis-specific
1436616_at	-0.31	-0.68	-0.50	0.003211729	269180	Inpp4a	inositol polyphosphate-4-phosphatase, type I
1421141_a_at	-0.37	-0.62	-0.50	0.00088086	108655	Foxp1	forkhead box P1
1420649_at	-0.35	-0.63	-0.49	0.001456307	11906	Zfhx3	zinc finger homeobox 3
1435935_at	-0.37	-0.61	-0.49	0.003348255	76792	2410131K14Rik	RIKEN cDNA 2410131K14 gene
1449615_s_at	-0.38	-0.60	-0.49	0.004020425	110611	Hdlbp	high density lipoprotein (HDL) binding protein
1418289_at	-0.61	-0.37	-0.49	0.000196724	18008	Nes	nestin
1438774_s_at	-0.29	-0.68	-0.49	0.00572028	70974	Pgm2l1	phosphoglucomutase 2-like 1
1417395_at	-0.58	-0.39	-0.49	0.001283066	16600	Klf4	Kruppel-like factor 4 (gut)
1433799_at	-0.30	-0.68	-0.49	0.011047806	108841	Rdh13	retinol dehydrogenase 13 (all-trans and 9-cis)
1453593_at	-0.65	-0.32	-0.49	0.002084489	73569	Vgll3	vestigial like 3 (Drosophila)
1417473_a_at	-0.59	-0.38	-0.49	0.000122421	106564	Ppcs	phosphopantothenoylcysteine synthetase
1438719_at	-0.33	-0.64	-0.48	0.00765702	26405	Map3k2	mitogen-activated protein kinase kinase kinase 2
1456643_at	-0.58	-0.38	-0.48	0.00251759	414108	9230114K14Rik	RIKEN cDNA 9230114K14 gene
1455048_at	-0.70	-0.27	-0.48	0.009886611	78908	Igsf3	immunoglobulin superfamily, member 3
1445881_at	-0.37	-0.59	-0.48	0.001473793	75683	2310035P21Rik	RIKEN cDNA 2310035P21 gene
1436194_at	-0.63	-0.33	-0.48	0.003347816	77619	Prelid2	PRELI domain containing 2
1439632_at	-0.60	-0.37	-0.48	0.001088011	14696	Gnb4	guanine nucleotide binding protein (G protein), beta 4
1439044_at	-0.61	-0.35	-0.48	0.000818717	30944	Zfp354c	zinc finger protein 354C
1431074_a_at	-0.19	-0.78	-0.48	0.007675472	71795	Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1
1442340_x_at	-0.86	-0.10	-0.48	0.017376996	16007	Cyr61	cysteine rich protein 61
1422580_at	-0.70	-0.26	-0.48	0.00560777	17896	Myl4	myosin, light polypeptide 4
1416686_at	-0.32	-0.63	-0.48	0.000782517	26432	Plod2	procollagen lysine, 2-oxoglutarate 5-dioxygenase 2
1435653_at	-0.25	-0.69	-0.47	0.007283193	54608	Abhd2	abhydrolase domain containing 2
1423061_at	-0.32	-0.63	-0.47	0.00411101	11877	Arvcf	armadillo repeat gene deleted in velo-cardio-facial syndrome
1435473_at	-0.12	-0.83	-0.47	0.004751594	241289	Ppp1r26	protein phosphatase 1, regulatory subunit 26
1437106_at	-0.58	-0.36	-0.47	0.004001631	214899	Kdm5a	lysine (K)-specific demethylase 5A
1427189_at	-0.65	-0.29	-0.47	0.041180563	23806	Arih1	ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosophila)
1428206_at	-0.63	-0.31	-0.47	0.012403995	52570	Ccdc69	coiled-coil domain containing 69
1455750_at	-0.63	-0.30	-0.47	0.014639152	241694	Ralgapa2	Ral GTPase activating protein, alpha subunit 2 (catalytic)
1424325_at	-0.29	-0.65	-0.47	0.046765389	77805	Esco1	establishment of cohesion 1 homolog 1 (S. cerevisiae)

1435564_at	-0.24	-0.69	-0.47	0.042659611	240055	Neurl1b	neuralized homolog 1b (Drosophila)
1434089_at	-0.34	-0.59	-0.46	0.000773444	104027	Synpo	synaptopodin
1426327_s_at	-0.22	-0.71	-0.46	0.001886152	109910	Zfp91	zinc finger protein 91
1426327_s_at	-0.22	-0.71	-0.46	0.001886152	664779	U05342	sequence U05342
1416910_at	-0.69	-0.23	-0.46	0.004063374	66148	Dnajc15	DnaJ (Hsp40) homolog, subfamily C, member 15
1427056_at	-0.29	-0.62	-0.46	0.001371693	235130	Adamts15	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 15
1428878_a_at	-0.32	-0.58	-0.45	0.012321935	71795	Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1
1424886_at	-0.61	-0.30	-0.45	0.009385111	19266	Ptprd	protein tyrosine phosphatase, receptor type, D
1456623_at	-0.60	-0.30	-0.45	0.016491231	22003	Tpm1	tropomyosin 1, alpha
1450990_at	-0.22	-0.68	-0.45	0.005432038	14734	Gpc3	glypican 3
1431792_a_at	-0.29	-0.62	-0.45	0.008049071	71728	Stk11ip	serine/threonine kinase 11 interacting protein
1453144_at	-0.60	-0.30	-0.45	0.044887753	66776	Pisd-ps3	phosphatidylserine decarboxylase, pseudogene 3
1445669_at	-0.66	-0.24	-0.45	0.003729207	24066	Spry4	sprouty homolog 4 (Drosophila)
1432057_a_at	-0.59	-0.31	-0.45	0.001720506	70779	Prdm5	PR domain containing 5
1457472_at	-0.62	-0.27	-0.44	0.040289427	227331	Gigyf2	GRB10 interacting GYF protein 2
1457823_at	-0.85	-0.03	-0.44	0.033613776	16007	Cyr61	cysteine rich protein 61
1419699_at	-0.62	-0.27	-0.44	0.020770004	68662	Scgb3a1	secretoglobin, family 3A, member 1
1438801_at	-0.69	-0.19	-0.44	0.031282623	103967	Dnm3	dynamin 3
1438012_at	-0.24	-0.63	-0.44	0.001199297	242083	Ppm1l	protein phosphatase 1 (formerly 2C)-like
1436446_at	-0.19	-0.68	-0.43	0.00825176	74177	2310007O11Rik	RIKEN cDNA 2310007O11 gene
1454855_at	-0.75	-0.12	-0.43	0.048292204	50791	Magi2	membrane associated guanylate kinase, WW and PDZ domain containing 2
1437118_at	-0.14	-0.73	-0.43	0.009328499	252870	Usp7	ubiquitin specific peptidase 7
1429656_at	-0.60	-0.26	-0.43	0.015065515	69288	Rhobtb1	Rho-related BTB domain containing 1
1428250_at	-0.27	-0.58	-0.43	0.000168292	76854	Gpr30	G protein-coupled receptor 30
1437462_x_at	-0.75	-0.09	-0.42	0.043655483	17388	Mmp15	matrix metallopeptidase 15
1419693_at	-0.63	-0.21	-0.42	0.005619665	140792	Colec12	collectin sub-family member 12
1440975_at	-0.66	-0.18	-0.42	0.008137286	67622	Mxra7	matrix-remodelling associated 7
1457881_at	-0.71	-0.12	-0.42	0.023480966	99031	Osbpl6	oxysterol binding protein-like 6
1415800_at	-0.65	-0.18	-0.42	0.00795882	14609	Gja1	gap junction protein, alpha 1
1417040_a_at	-0.59	-0.23	-0.41	0.022085282	51800	Bok	BCL2-related ovarian killer protein
1438263_at	-0.23	-0.59	-0.41	0.030845622	240185	9430020K01Rik	RIKEN cDNA 9430020K01 gene
1456674_at	-0.64	-0.19	-0.41	0.041081305	100503583	Fsbp	fibrinogen silencer binding protein
1456674_at	-0.64	-0.19	-0.41	0.041081305	623474	Rad54b	RAD54 homolog B (S. cerevisiae)
1428834_at	-0.20	-0.62	-0.41	0.008581293	319520	Dusp4	dual specificity phosphatase 4
1438732_at	-0.60	-0.22	-0.41	0.044455628	100042480	Nhsl2	NHS-like 2
1449152_at	-0.60	-0.22	-0.41	0.006292242	12579	Cdkn2b	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)
1454823_at	-0.19	-0.63	-0.41	0.01130486	207615	Wdr37	WD repeat domain 37
1418129_at	-0.70	-0.12	-0.41	0.004093823	74754	Dhcr24	24-dehydrocholesterol reductase
1456762_at	-0.62	-0.19	-0.41	0.039646586	231931	Gimap6	GTPase, IMAP family member 6
1420947_at	-0.22	-0.59	-0.40	0.018770797	22589	Atrx	alpha thalassemia/mental retardation syndrome X-linked homolog (human)
1432499_a_at	-0.11	-0.70	-0.40	0.027912282	63958	Ube4b	ubiquitination factor E4B, UFD2 homolog (S. cerevisiae)
1422806_x_at	-0.58	-0.22	-0.40	0.031858836	71777	Ing3	inhibitor of growth family, member 3
1433618_at	-0.11	-0.69	-0.40	0.007452057	109299	C330006A16Rik	RIKEN cDNA C330006A16 gene
1438945_x_at	-0.61	-0.20	-0.40	0.014001136	14609	Gja1	gap junction protein, alpha 1
1449314_at	-0.03	-0.77	-0.40	0.012911784	22762	Zfpm2	zinc finger protein, multitype 2
1449244_at	-0.60	-0.19	-0.40	0.014883813	12558	Cdh2	cadherin 2
1421255_a_at	-0.16	-0.62	-0.39	0.020534201	29867	Cabp1	calcium binding protein 1
1421007_at	-0.18	-0.60	-0.39	0.020399259	94216	Col4a6	collagen, type IV, alpha 6
1427320_at	-0.65	-0.12	-0.39	0.045249733	100044236	Copg2as2	coatomer protein complex, subunit gamma 2, antisense 2
1435468_at	-0.11	-0.66	-0.39	0.02972005	97440	B3gnt9	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9
1442700_at	-0.08	-0.69	-0.38	0.04498397	18578	Pde4b	phosphodiesterase 4B, cAMP specific
1433662_s_at	-0.19	-0.58	-0.38	0.003389646	21858	Timp2	tissue inhibitor of metalloproteinase 2
1418030_at	-0.58	-0.17	-0.38	0.011207885	108116	Slco3a1	solute carrier organic anion transporter family, member 3a1
1458685_at	-0.64	-0.10	-0.37	0.047675525	56784	Ralgapa1	Ral GTPase activating protein, alpha subunit 1
1459104_at	-0.10	-0.62	-0.36	0.039833224	12237	Bub3	budding uninhibited by benzimidazoles 3 homolog (S. cerevisiae)
1424598_at	-0.05	-0.66	-0.36	0.02238778	13209	Ddx6	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6
1433493_at	-0.08	-0.62	-0.35	0.009360752	108958	Fam73b	family with sequence similarity 73, member B
1446844_at	-0.05	-0.63	-0.34	0.030696693	66433	Chchd7	coiled-coil-helix-coiled-coil-helix domain containing 7
1449461_at	-0.07	-0.59	-0.33	0.040732364	63954	Rbp7	retinol binding protein 7, cellular

Supplemental Table II: All upregulated transcripts in brain microvasculature of *Notch3*$^{-/-}$ vs WT

Affymetrix probe set ID	Cerebrum N3$^{-/-}$ vs WT (log2)	Cerebellum N3$^{-/-}$ vs WT (log2)	Average fold (log2)	P value	ENTREZ ID	Symbol	Gene Name
1438936_s_at	10.66	9.93	10.30	7.17E-14	58809	Rnase4	ribonuclease, RNase A family 4
1438936_s_at	10.66	9.93	10.30	7.17E-14	11727	Ang	angiogenin, ribonuclease, RNase A family, 5
1438937_x_at	9.08	8.34	8.71	4.79E-12	11727	Ang	angiogenin, ribonuclease, RNase A family, 5
1438937_x_at	9.08	8.34	8.71	4.79E-12	58809	Rnase4	ribonuclease, RNase A family 4
1437128_a_at	6.22	5.30	5.76	7.64E-09	240041	Zfp945	zinc finger protein 945
1421144_at	4.51	5.05	4.78	5.53E-10	77945	Rpgrip1	retinitis pigmentosa GTPase regulator interacting protein 1
1460628_at	3.67	3.49	3.58	1.58E-08	193838	Eme2	essential meiotic endonuclease 1 homolog 2 (S. pombe)
1450717_at	3.75	3.23	3.49	2.07E-09	11727	Ang	angiogenin, ribonuclease, RNase A family, 5
1458659_at	2.42	2.94	2.68	1.56E-06	100039246	Plac9b	placenta specific 9b
1458659_at	2.42	2.94	2.68	1.56E-06	100039175	Gm9780	predicted gene 9780
1458659_at	2.42	2.94	2.68	1.56E-06	211623	Plac9a	placenta specific 9a
1437614_x_at	2.40	2.70	2.55	1.48E-07	224454	Zdhhc14	zinc finger, DHHC domain containing 14
1430886_at	2.56	2.44	2.50	5.82E-09	76633	1700112E06Rik	RIKEN cDNA 1700112E06 gene
1421525_a_at	2.92	2.02	2.47	0.017239879	17951	Naip5	NLR family, apoptosis inhibitory protein 5
1419635_at	2.29	2.57	2.43	0.000338354	67392	4833420G17Rik	RIKEN cDNA 4833420G17 gene
1428738_a_at	2.64	2.22	2.43	3.91E-08	100039192	Tmem254c	transmembrane protein 254c
1428738_a_at	2.64	2.22	2.43	3.91E-08	66039	Tmem254a	transmembrane protein 254a
1428738_a_at	2.64	2.22	2.43	3.91E-08	100039257	Tmem254b	transmembrane protein 254b
1455735_at	2.35	2.32	2.33	2.63E-08	252903	Ap1s3	adaptor-related protein complex AP-1, sigma 3
1418172_at	2.55	2.09	2.32	7.86E-09	15199	Hebp1	heme binding protein 1
1454674_at	2.14	2.37	2.25	8.13E-07	235180	Fez1	fasciculation and elongation protein zeta 1 (zygin I)
1418908_at	2.07	2.37	2.22	6.86E-05	18484	Pam	peptidylglycine alpha-amidating monooxygenase
1422527_at	2.60	1.77	2.18	4.83E-06	14998	H2-DMa	histocompatibility 2, class II, locus DMa
1453109_at	2.35	2.02	2.18	0.007638684	77041	Arsk	arylsulfatase K
1428692_at	2.02	2.31	2.16	9.25E-06	68695	Hddc3	HD domain containing 3
1444589_at	2.19	2.00	2.09	2.56E-08	240038	Gm4944	predicted gene 4944
1452590_a_at	1.87	2.31	2.09	3.38E-08	211623	Plac9a	placenta specific 9a
1452590_a_at	1.87	2.31	2.09	3.38E-08	100039246	Plac9b	placenta specific 9b
1452590_a_at	1.87	2.31	2.09	3.38E-08	100039175	Gm9780	predicted gene 9780
1415856_at	2.59	1.48	2.03	0.002368252	13723	Emb	embigin
1421732_at	2.86	1.05	1.95	0.000245537	14659	Glrp1	glutamine repeat protein 1
1424965_at	2.48	1.41	1.94	0.00022348	107321	Lpxn	leupaxin
1425597_a_at	2.19	1.68	1.94	4.67E-07	19317	Qk	quaking
1416125_at	1.98	1.86	1.92	0.000624754	14229	Fkbp5	FK506 binding protein 5
1457026_at	3.02	0.67	1.85	0.010430986	239759	Liph	lipase, member H
1422875_at	2.43	1.17	1.80	0.001060988	12523	Cd84	CD84 antigen
1435943_at	0.80	2.74	1.77	0.01391686	13479	Dpep1	dipeptidase 1 (renal)
1452837_at	1.68	1.80	1.74	0.000342236	64898	Lpin2	lipin 2
1436853_a_at	1.80	1.68	1.74	0.009997224	20617	Snca	synuclein, alpha
1427451_a_at	1.61	1.80	1.71	1.72E-07	193217	BC018473	cDNA sequence BC018473
1434585_at	1.73	1.65	1.69	5.62E-09	68842	Tulp4	tubby like protein 4
1436074_at	1.20	2.10	1.65	0.006004297	243910	Nfkbid	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, delta
1420357_s_at	1.80	1.38	1.59	0.037643645	22446	Xlr3c	X-linked lymphocyte-regulated 3C
1420357_s_at	1.80	1.38	1.59	0.037643645	22445	Xlr3a	X-linked lymphocyte-regulated 3A
1420357_s_at	1.80	1.38	1.59	0.037643645	574437	Xlr3b	X-linked lymphocyte-regulated 3B
1435984_at	1.47	1.68	1.57	6.79E-05	22700	Zfp40	zinc finger protein 40
1448590_at	1.46	1.64	1.55	7.72E-07	12833	Col6a1	collagen, type VI, alpha 1
1451584_at	2.09	0.98	1.53	0.000719141	171285	Havcr2	hepatitis A virus cellular receptor 2
1419561_at	1.53	1.50	1.52	0.002736885	20302	Ccl3	chemokine (C-C motif) ligand 3
1453474_at	2.08	0.91	1.50	0.000402296	67477	Abhd15	abhydrolase domain containing 15
1452836_at	1.51	1.47	1.49	0.000176205	64898	Lpin2	lipin 2
1450972_at	1.49	1.42	1.45	4.78E-05	67290	3110040N11Rik	RIKEN cDNA 3110040N11 gene
1426260_a_at	1.94	0.94	1.44	0.000155263	394432	Ugt1a7c	UDP glucuronosyltransferase 1 family, polypeptide A7C
1426260_a_at	1.94	0.94	1.44	0.000155263	394434	Ugt1a9	UDP glucuronosyltransferase 1 family, polypeptide A9
1426260_a_at	1.94	0.94	1.44	0.000155263	394430	Ugt1a10	UDP glycosyltransferase 1 family, polypeptide A10
1426260_a_at	1.94	0.94	1.44	0.000155263	394433	Ugt1a5	UDP glucuronosyltransferase 1 family, polypeptide A5
1426260_a_at	1.94	0.94	1.44	0.000155263	394435	Ugt1a6b	UDP glucuronosyltransferase 1 family, polypeptide A6B
1426260_a_at	1.94	0.94	1.44	0.000155263	394436	Ugt1a1	UDP glucuronosyltransferase 1 family, polypeptide A1
1426260_a_at	1.94	0.94	1.44	0.000155263	22236	Ugt1a2	UDP glucuronosyltransferase 1 family, polypeptide A2
1426260_a_at	1.94	0.94	1.44	0.000155263	94284	Ugt1a6a	UDP glucuronosyltransferase 1 family, polypeptide A6A
1426260_a_at	1.94	0.94	1.44	0.000155263	100048662	LOC100048662	UDP-glucuronosyltransferase 1-9-like
1426607_at	1.51	1.33	1.42	0.003811256	633640	Gm7120	predicted gene 7120
1438975_x_at	1.36	1.43	1.40	1.09E-06	224454	Zdhhc14	zinc finger, DHHC domain containing 14
1426472_at	1.49	1.29	1.39	0.000289519	22710	Zfp52	zinc finger protein 52
1436397_at	1.79	0.98	1.38	0.000349996	212937	Tifab	TRAF-interacting protein with forkhead-associated domain, family member B
1439956_at	1.98	0.77	1.38	0.000559854	69774	Ms4a6b	membrane-spanning 4-domains, subfamily A, member 6B
1446316_at	1.60	1.13	1.37	0.0019904	64898	Lpin2	lipin 2
1446244_at	1.34	1.36	1.35	0.000240941	414872	Zyg11b	zyg-ll family member B, cell cycle regulator
1419598_at	1.68	1.01	1.34	0.001575052	68774	Ms4a6d	membrane-spanning 4-domains, subfamily A, member 6D
1426261_s_at	2.08	0.58	1.33	0.001643298	394435	Ugt1a6b	UDP glucuronosyltransferase 1 family, polypeptide A6B

1426261_s_at	2.08	0.58	1.33	0.001643298	394436	Ugt1a1	UDP glucuronosyltransferase 1 family, polypeptide A1
1426261_s_at	2.08	0.58	1.33	0.001643298	22236	Ugt1a2	UDP glucuronosyltransferase 1 family, polypeptide A2
1426261_s_at	2.08	0.58	1.33	0.001643298	394430	Ugt1a10	UDP glycosyltransferase 1 family, polypeptide A10
1426261_s_at	2.08	0.58	1.33	0.001643298	94284	Ugt1a6a	UDP glucuronosyltransferase 1 family, polypeptide A6A
1426261_s_at	2.08	0.58	1.33	0.001643298	100048662	LOC100048662	UDP-glucuronosyltransferase 1-9-like
1426261_s_at	2.08	0.58	1.33	0.001643298	394434	Ugt1a9	UDP glucuronosyltransferase 1 family, polypeptide A9
1426261_s_at	2.08	0.58	1.33	0.001643298	394432	Ugt1a7c	UDP glucuronosyltransferase 1 family, polypeptide A7C
1426261_s_at	2.08	0.58	1.33	0.001643298	394433	Ugt1a5	UDP glucuronosyltransferase 1 family, polypeptide A5
1426471_at	1.28	1.37	1.33	9.55E-09	22710	Zfp52	zinc finger protein 52
1455132_at	1.97	0.67	1.32	0.019139606	320484	Rasal3	RAS protein activator like 3
1445104_at	1.94	0.70	1.32	0.002637758	319711	E230029C05Rik	RIKEN cDNA E230029C05 gene
1419004_s_at	1.64	0.99	1.32	0.000487367	12047	Bcl2a1d	B cell leukemia/lymphoma 2 related protein A1d
1419004_s_at	1.64	0.99	1.32	0.000487367	12044	Bcl2a1a	B cell leukemia/lymphoma 2 related protein A1a
1419004_s_at	1.64	0.99	1.32	0.000487367	12045	Bcl2a1b	B cell leukemia/lymphoma 2 related protein A1b
1418003_at	1.01	1.63	1.32	0.000551981	66214	Rgcc	regulator of cell cycle
1418203_at	1.36	1.26	1.31	3.03E-05	58801	Pmaip1	phorbol-12-myristate-13-acetate-induced protein 1
1417266_at	1.67	0.91	1.29	0.000398855	20305	Ccl6	chemokine (C-C motif) ligand 6
1426464_at	1.23	1.34	1.29	0.046201091	217166	Nr1d1	nuclear receptor subfamily 1, group D, member 1
1428975_at	2.16	0.37	1.26	0.024424997	66329	Susd3	sushi domain containing 3
1427496_at	1.67	0.84	1.26	0.000138753	99100	Cep152	centrosomal protein 152
1440209_at	1.50	0.98	1.24	0.000282016	72925	01-Mar	membrane-associated ring finger (C3HC4) 1
1416827_at	1.62	0.86	1.24	0.001580431	21391	Tbxas1	thromboxane A synthase 1, platelet
1421221_at	1.61	0.86	1.23	0.005440902	170752	Bco2	beta-carotene oxygenase 2
1417936_at	1.67	0.77	1.22	0.005081813	20308	Ccl9	chemokine (C-C motif) ligand 9
1424783_a_at	1.76	0.68	1.22	0.000945224	94284	Ugt1a6a	UDP glucuronosyltransferase 1 family, polypeptide A6A
1424783_a_at	1.76	0.68	1.22	0.000945224	394433	Ugt1a5	UDP glucuronosyltransferase 1 family, polypeptide A5
1424783_a_at	1.76	0.68	1.22	0.000945224	22236	Ugt1a2	UDP glucuronosyltransferase 1 family, polypeptide A2
1424783_a_at	1.76	0.68	1.22	0.000945224	394430	Ugt1a10	UDP glycosyltransferase 1 family, polypeptide A10
1424783_a_at	1.76	0.68	1.22	0.000945224	394435	Ugt1a6b	UDP glucuronosyltransferase 1 family, polypeptide A6B
1424783_a_at	1.76	0.68	1.22	0.000945224	394432	Ugt1a7c	UDP glucuronosyltransferase 1 family, polypeptide A7C
1424783_a_at	1.76	0.68	1.22	0.000945224	394436	Ugt1a1	UDP glucuronosyltransferase 1 family, polypeptide A1
1424783_a_at	1.76	0.68	1.22	0.000945224	100048662	LOC100048662	UDP-glucuronosyltransferase 1-9-like
1424783_a_at	1.76	0.68	1.22	0.000945224	394434	Ugt1a9	UDP glucuronosyltransferase 1 family, polypeptide A9
1420249_s_at	1.50	0.92	1.21	0.000962504	20305	Ccl6	chemokine (C-C motif) ligand 6
1415857_at	1.36	1.06	1.21	0.000613215	13723	Emb	embigin
1428018_a_at	1.62	0.77	1.20	0.002955768	140497	AF251705	cDNA sequence AF251705
1436528_at	1.18	1.22	1.20	0.001284882	107250	Kazald1	Kazal-type serine peptidase inhibitor domain 1
1418826_at	1.59	0.80	1.19	0.000416674	69774	Ms4a6b	membrane-spanning 4-domains, subfamily A, member 6B
1452250_a_at	1.02	1.34	1.18	1.98E-05	12834	Col6a2	collagen, type VI, alpha 2
1427076_at	1.46	0.87	1.17	0.000341813	17476	Mpeg1	macrophage expressed gene 1
1436512_at	1.61	0.71	1.16	0.001202945	320982	Arl4c	ADP-ribosylation factor-like 4C
1434903_s_at	1.64	0.66	1.15	0.009880241	107527	Il1rl2	interleukin 1 receptor-like 2
1444546_at	1.97	0.33	1.15	0.010071556	212937	Tifab	TRAF-interacting protein with forkhead-associated domain, family member B
1456923_at	1.36	0.91	1.14	0.020394201	226025	Trpm3	transient receptor potential cation channel, subfamily M, member 3
1419609_at	1.98	0.27	1.13	0.038629172	12768	Ccr1	chemokine (C-C motif) receptor 1
1451006_at	1.10	1.14	1.12	0.001820219	22436	Xdh	xanthine dehydrogenase
1430986_at	1.08	1.15	1.12	5.06E-05	23874	Farsb	phenylalanyl-tRNA synthetase, beta subunit
1428242_at	1.57	0.66	1.11	0.008264558	70719	Hmha1	histocompatibility (minor) HA-1
1416639_at	1.52	0.70	1.11	0.001719479	56485	Slc2a5	solute carrier family 2 (facilitated glucose transporter), member 5
1429954_at	1.50	0.71	1.11	0.002062627	73149	Clec4a3	C-type lectin domain family 4, member a3
1460290_at	1.38	0.81	1.09	0.000619528	64898	Lpin2	lipin 2
1426979_at	1.53	0.63	1.08	0.000360569	208104	Mlxip	MLX interacting protein
1425736_at	1.47	0.68	1.08	0.011151838	12493	Cd37	CD37 antigen
1426988_at	1.05	1.10	1.07	0.006739083	232539	Klhdc5	kelch domain containing 5
1421028_a_at	1.36	0.78	1.07	0.004732633	17260	Mef2c	myocyte enhancer factor 2C
1453070_at	0.97	1.15	1.06	0.00648265	219228	Pcdh17	protocadherin 17
1422010_at	1.55	0.57	1.06	0.000750979	170743	Tlr7	toll-like receptor 7
1421492_at	1.46	0.65	1.06	0.001796308	54486	Hpgds	hematopoietic prostaglandin D synthase
1417976_at	0.91	1.20	1.05	1.50E-05	11486	Ada	adenosine deaminase
1451941_a_at	1.24	0.84	1.04	0.006586268	14130	Fcgr2b	Fc receptor, IgG, low affinity IIb
1433719_at	1.33	0.75	1.04	0.001542753	331004	Slc9a9	solute carrier family 9 (sodium/hydrogen exchanger), member 9
1455033_at	1.38	0.69	1.04	0.00072786	329739	Fam102b	family with sequence similarity 102, member B
1419599_s_at	1.38	0.69	1.03	0.002106594	68774	Ms4a6d	membrane-spanning 4-domains, subfamily A, member 6D
1419206_at	1.56	0.51	1.03	0.004716318	12493	Cd37	CD37 antigen
1440245_at	1.88	0.19	1.03	0.030962377	78317	Ccdc88b	coiled-coil domain containing 88B
1418153_at	0.89	1.15	1.02	0.000736608	16772	Lama1	laminin, alpha 1
1455967_at	1.07	0.98	1.02	0.024534572	20411	Sorbs1	sorbin and SH3 domain containing 1
1434955_at	1.51	0.52	1.01	0.001702343	72925	01-Mar	membrane-associated ring finger (C3HC4) 1
1428458_at	1.06	0.96	1.01	1.63E-05	67724	Pop1	processing of precursor 1, ribonuclease P/MRP family, (S. cerevisiae)
1419194_s_at	1.14	0.86	1.00	0.001581012	63986	Gmfg	glia maturation factor, gamma
1419194_s_at	1.14	0.86	1.00	0.001581012	100040018	Gm9835	predicted pseudogene 9835
1419905_s_at	1.33	0.67	1.00	0.002720759	15446	Hpgd	hydroxyprostaglandin dehydrogenase 15 (NAD)
1437911_at	0.98	1.02	1.00	1.40E-07	319615	Zfp944	zinc finger protein 944
1434828_at	1.31	0.67	0.99	0.000328063	329739	Fam102b	family with sequence similarity 102, member B
1423937_at	0.97	1.00	0.98	4.57E-06	69259	Kctd5	potassium channel tetramerisation domain containing 5
1456411_at	0.83	1.13	0.98	0.000297855	269955	Rccd1	RCC1 domain containing 1
1430534_at	1.31	0.65	0.98	0.00059916	78416	Rnase6	ribonuclease, RNase A family, 6

1435477_s_at	1.25	0.70	0.97	0.007315994	14130	Fcgr2b	Fc receptor, IgG, low affinity IIb
1448028_at	0.97	0.97	0.97	1.12E-07	224617	Tbc1d24	TBC1 domain family, member 24
1449580_s_at	1.68	0.24	0.96	0.033392493	15000	H2-DMb2	histocompatibility 2, class II, locus Mb2
1449580_s_at	1.68	0.24	0.96	0.033392493	14999	H2-DMb1	histocompatibility 2, class II, locus Mb1
1455426_at	0.97	0.96	0.96	0.005700355	13837	Epha3	Eph receptor A3
1421366_at	1.38	0.54	0.96	0.026417619	23845	Clec5a	C-type lectin domain family 5, member a
1449222_at	1.37	0.53	0.95	0.015696923	50498	Ebi3	Epstein-Barr virus induced gene 3
1449846_at	1.07	0.82	0.95	0.033173314	53876	Ear3	eosinophil-associated, ribonuclease A family, member 3
1449846_at	1.07	0.82	0.95	0.033173314	503845	Ear12	eosinophil-associated, ribonuclease A family, member 12
1449846_at	1.07	0.82	0.95	0.033173314	13587	Ear2	eosinophil-associated, ribonuclease A family, member 2
1435213_at	0.89	1.00	0.94	8.80E-05	105193	Nhlrc1	NHL repeat containing 1
1431569_a_at	0.81	1.08	0.94	0.004654604	72585	Lypd1	Ly6/Plaur domain containing 1
1457065_at	1.89	-0.01	0.94	0.031885009	22268	Upk1b	uroplakin 1B
1445647_at	1.23	0.64	0.93	0.020837598	99627	AI447881	expressed sequence AI447881
1449099_at	1.27	0.60	0.93	0.000135407	80877	Lrba	LPS-responsive beige-like anchor
1435292_at	0.97	0.89	0.93	0.003438294	210789	Tbc1d4	TBC1 domain family, member 4
1435918_at	0.82	1.03	0.93	0.013077582	268709	Fam107a	family with sequence similarity 107, member A
1456807_at	0.95	0.89	0.92	0.001035681	105651	Ppp1r3e	protein phosphatase 1, regulatory (inhibitor) subunit 3E
1426413_at	0.00	1.84	0.92	0.028295238	18012	Neurod1	neurogenic differentiation 1
1452063_at	0.76	1.07	0.92	0.003567977	73680	Zbtb8a	zinc finger and BTB domain containing 8a
1426947_x_at	0.63	1.20	0.92	0.001410026	12834	Col6a2	collagen, type VI, alpha 2
1435188_at	0.63	1.18	0.90	0.040239345	229599	Gm129	predicted gene 129
1456937_at	1.05	0.76	0.90	0.001792784	381409	Cdh26	cadherin-like 26
1449858_at	1.05	0.73	0.89	0.032825055	12524	Cd86	CD86 antigen
1453591_at	0.74	1.03	0.89	3.45E-05	70544	Tmem242	transmembrane protein 242
1439111_at	0.84	0.93	0.89	6.49E-05	21807	Tsc22d1	TSC22 domain family, member 1
1439111_at	0.84	0.93	0.89	6.49E-05	100503222	Gm19597	predicted gene, 19597
1455464_x_at	1.52	0.26	0.89	0.031401488	22268	Upk1b	uroplakin 1B
1434329_s_at	0.96	0.81	0.89	8.84E-05	68465	Adipor2	adiponectin receptor 2
1460273_a_at	1.14	0.62	0.88	0.022654492	17948	Naip2	NLR family, apoptosis inhibitory protein 2
1417653_at	-0.09	1.85	0.88	0.042006067	19293	Pvalb	parvalbumin
1436570_at	1.26	0.50	0.88	0.000664922	94212	Pag1	phosphoprotein associated with glycosphingolipid microdomains 1
1427012_at	0.79	0.96	0.88	5.52E-05	14768	Lancl1	LanC (bacterial lantibiotic synthetase component C)-like 1
1433964_s_at	1.28	0.47	0.88	0.007431987	108101	Fermt3	fermitin family homolog 3 (Drosophila)
1419289_a_at	1.34	0.40	0.87	0.004320402	20972	Syngr1	synaptogyrin 1
1452948_at	1.18	0.55	0.87	0.001856507	69769	Tnfaip8l2	tumor necrosis factor, alpha-induced protein 8-like 2
1422477_at	0.88	0.84	0.86	0.000318569	63955	Cables1	CDK5 and Abl enzyme substrate 1
1452272_a_at	0.94	0.78	0.86	1.13E-07	11692	Gfer	growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)
1434945_at	1.25	0.46	0.85	0.007540816	270084	Lpcat2	lysophosphatidylcholine acyltransferase 2
1435722_at	0.73	0.97	0.85	0.02661998	14802	Gria4	glutamate receptor, ionotropic, AMPA4 (alpha 4)
1438123_at	0.83	0.87	0.85	0.019390024	378466	Gm10033	predicted gene 10033
1438123_at	0.83	0.87	0.85	0.019390024	100505118	LOC100505118	uncharacterized LOC100505118
1440559_at	1.27	0.43	0.85	0.004648716	15365	Hmga2-ps1	high mobility group AT-hook 2, pseudogene 1
1416531_at	0.80	0.90	0.85	0.000492039	14873	Gsto1	glutathione S-transferase omega 1
1459827_x_at	0.69	1.01	0.85	0.006552411	192236	Hps1	Hermansky-Pudlak syndrome 1 homolog (human)
1456328_at	1.36	0.34	0.85	0.02867401	242248	Bank1	B cell scaffold protein with ankyrin repeats 1
1420150_at	1.07	0.63	0.85	0.000840159	74646	Spsb1	splA/ryanodine receptor domain and SOCS box containing 1
1434203_at	0.72	0.97	0.85	0.000262231	268709	Fam107a	family with sequence similarity 107, member A
1422298_at	0.98	0.71	0.85	0.002738562	71386	Krtap28-13	keratin associated protein 28-13
1420575_at	0.69	1.00	0.84	0.006201462	17751	Mt3	metallothionein 3
1426715_s_at	1.35	0.32	0.83	0.004354074	52466	Slc46a1	solute carrier family 46, member 1
1435487_at	-0.06	1.72	0.83	0.023668044	14804	Grid2	glutamate receptor, ionotropic, delta 2
1426787_at	0.92	0.75	0.83	0.002267693	100861749	LOC100861749	protein SFI1 homolog
1426787_at	0.92	0.75	0.83	0.002267693	78887	Sfi1	Sfi1 homolog, spindle assembly associated (yeast)
1418807_at	0.71	0.95	0.83	0.015417316	67304	3110070M22Rik	RIKEN cDNA 3110070M22 gene
1455332_x_at	1.04	0.61	0.82	0.005188445	14130	Fcgr2b	Fc receptor, IgG, low affinity IIb
1456036_x_at	0.83	0.82	0.82	0.00038825	14873	Gsto1	glutathione S-transferase omega 1
1448534_at	1.54	0.08	0.81	0.044426633	19261	Sirpa	signal-regulatory protein alpha
1436076_at	1.28	0.34	0.81	0.009695679	224997	Dlgap1	discs, large (Drosophila) homolog-associated protein 1
1458459_a_at	1.10	0.51	0.81	0.001830428	319711	E230029C05Rik	RIKEN cDNA E230029C05 gene
1433266_at	0.86	0.75	0.81	0.00613776	70241	2810416A17Rik	RIKEN cDNA 2810416A17 gene
1422771_at	0.67	0.94	0.80	0.000779146	17130	Smad6	SMAD family member 6
1439397_at	0.92	0.69	0.80	0.004966337	14260	Fmn1	formin 1
1417184_s_at	0.34	1.27	0.80	0.046613815	100503605	Beta-s	hemoglobin subunit beta-1-like
1417184_s_at	0.34	1.27	0.80	0.046613815	15129	Hbb-b1	hemoglobin, beta adult major chain
1417184_s_at	0.34	1.27	0.80	0.046613815	15130	Hbb-b2	hemoglobin, beta adult minor chain
1460011_at	1.00	0.61	0.80	0.00974523	232174	Cyp26b1	cytochrome P450, family 26, subfamily b, polypeptide 1
1415871_at	0.68	0.92	0.80	0.000429412	21810	Tgfbi	transforming growth factor, beta induced
1430979_a_at	0.79	0.80	0.79	0.019672575	21672	Prdx2	peroxiredoxin 2
1419636_at	0.85	0.73	0.79	0.000790273	67392	4833420G17Rik	RIKEN cDNA 4833420G17 gene
1428394_at	1.14	0.43	0.79	0.001536911	241296	Lrrc8a	leucine rich repeat containing 8A
1428394_at	1.14	0.43	0.79	0.001536911	227696	Phyhd1	phytanoyl-CoA dioxygenase domain containing 1
1433586_at	0.97	0.60	0.79	6.32E-05	68799	Rgmb	RGM domain family, member B
1451987_at	0.97	0.60	0.79	0.010203824	216869	Arrb2	arrestin, beta 2
1460121_at	0.79	0.78	0.79	3.66E-06	399612	9630010G10Rik	RIKEN cDNA 9630010G10 gene
1435896_at	0.79	0.78	0.78	0.001777846	94279	Sfxn2	sideroflexin 2
1454788_at	1.20	0.36	0.78	0.007065726	320982	Arl4c	ADP-ribosylation factor-like 4C

1422643_at	0.57	0.98	0.78	0.009413551	59012	Moxd1	monooxygenase, DBH-like 1
1428455_at	0.59	0.96	0.78	0.004335871	12818	Col14a1	collagen, type XIV, alpha 1
1425546_a_at	1.05	0.50	0.78	0.000295871	20818	Srprb	signal recognition particle receptor, B subunit
1425546_a_at	1.05	0.50	0.78	0.000295871	22041	Trf	transferrin
1416514_a_at	0.90	0.65	0.77	0.000718791	14086	Fscn1	fascin homolog 1, actin bundling protein (Strongylocentrotus purpuratus)
1452016_at	1.14	0.41	0.77	0.003723215	11690	Alox5ap	arachidonate 5-lipoxygenase activating protein
1423915_at	0.77	0.76	0.77	0.000354343	320078	Olfml2b	olfactomedin-like 2B
1427883_a_at	0.71	0.82	0.77	0.000102634	12825	Col3a1	collagen, type III, alpha 1
1424265_at	1.28	0.25	0.77	0.012957649	74091	Npl	N-acetylneuraminate pyruvate lyase
1451344_at	1.16	0.37	0.76	0.006140084	231633	Tmem119	transmembrane protein 119
1460431_at	1.10	0.43	0.76	0.003919254	14537	Gcnt1	glucosaminyl (N-acetyl) transferase 1, core 2
1437270_a_at	0.83	0.70	0.76	0.024170772	56708	Clcf1	cardiotrophin-like cytokine factor 1
1417971_at	0.77	0.75	0.76	0.000113707	106582	Nrm	nurim (nuclear envelope membrane protein)
1456887_at	1.05	0.47	0.76	0.026942845	14747	Cmklr1	chemokine-like receptor 1
1428175_at	0.63	0.88	0.76	0.000153036	72745	Tmem161b	transmembrane protein 161B
1427168_a_at	0.67	0.84	0.75	0.002948397	12818	Col14a1	collagen, type XIV, alpha 1
1449164_at	1.16	0.35	0.75	0.014659618	12514	Cd68	CD68 antigen
1440773_at	1.02	0.49	0.75	0.00812278	382010	Cep44	centrosomal protein 44
1426714_at	1.02	0.48	0.75	0.001265565	52466	Slc46a1	solute carrier family 46, member 1
1423414_at	1.20	0.30	0.75	0.006067912	19224	Ptgs1	prostaglandin-endoperoxide synthase 1
1458399_at	1.42	0.08	0.75	0.044921694	237387	Lrrc3	leucine rich repeat containing 3
1455263_at	1.00	0.49	0.75	0.003913126	210808	Lacc1	laccase (multicopper oxidoreductase) domain containing 1
1433963_a_at	1.09	0.40	0.74	0.00466218	108101	Fermt3	fermitin family homolog 3 (Drosophila)
1425656_a_at	0.43	1.05	0.74	0.011854741	108100	Baiap2	brain-specific angiogenesis inhibitor 1-associated protein 2
1417381_at	1.01	0.48	0.74	0.002415464	12259	C1qa	complement component 1, q subcomponent, alpha polypeptide
1419184_a_at	0.48	1.00	0.74	0.000145672	14200	Fhl2	four and a half LIM domains 2
1449454_at	1.01	0.47	0.74	0.016004081	12182	Bst1	bone marrow stromal cell antigen 1
1430191_at	0.89	0.58	0.73	0.002957453	71603	9130004J05Rik	RIKEN cDNA 9130004J05 gene
1448201_at	0.46	1.00	0.73	0.001444311	20319	Sfrp2	secreted frizzled-related protein 2
1423887_a_at	0.86	0.60	0.73	5.59E-06	71718	Telo2	TEL2, telomere maintenance 2, homolog (S. cerevisiae)
1418842_at	1.06	0.41	0.73	0.002410172	15163	Hcls1	hematopoietic cell specific Lyn substrate 1
1424872_at	0.73	0.74	0.73	1.58E-05	69504	Zfp932	zinc finger protein 932
1422637_at	1.18	0.28	0.73	0.037984221	54354	Rassf5	Ras association (RalGDS/AF-6) domain family member 5
1450019_at	1.38	0.08	0.73	0.040891649	13051	Cx3cr1	chemokine (C-X3-C) receptor 1
1417121_at	0.03	1.43	0.73	0.016615593	14399	Gabra6	gamma-aminobutyric acid (GABA) A receptor, subunit alpha 6
1420404_at	1.25	0.21	0.73	0.016155425	12524	Cd86	CD86 antigen
1442094_at	0.80	0.65	0.72	0.004777255	66262	Ing5	inhibitor of growth family, member 5
1450065_at	1.15	0.29	0.72	0.026658701	11513	Adcy7	adenylate cyclase 7
1419692_a_at	1.11	0.33	0.72	0.005691544	17001	Ltc4s	leukotriene C4 synthase
1423888_at	0.73	0.70	0.72	1.59E-05	71718	Telo2	TEL2, telomere maintenance 2, homolog (S. cerevisiae)
1427884_at	0.63	0.80	0.71	0.001398815	12825	Col3a1	collagen, type III, alpha 1
1420819_at	1.13	0.30	0.71	0.006313602	20491	Sla	src-like adaptor
1450971_at	0.77	0.65	0.71	0.000429117	17873	Gadd45b	growth arrest and DNA-damage-inducible 45 beta
1429214_at	0.38	1.04	0.71	0.006245632	77794	Adamtsl2	ADAMTS-like 2
1417300_at	0.86	0.55	0.71	0.005653291	100340	Smpdl3b	sphingomyelin phosphodiesterase, acid-like 3B
1441516_a_at	0.68	0.73	0.71	0.043755106	319772	C130050O18Rik	RIKEN cDNA C130050O18 gene
1449131_s_at	0.98	0.43	0.71	0.005103458	12479	Cd1d1	CD1d1 antigen
1455455_at	0.81	0.59	0.70	0.022771006	320302	Glt28d2	glycosyltransferase 28 domain containing 2
1448819_at	0.62	0.78	0.70	0.004970669	67204	Eif2s2	eukaryotic translation initiation factor 2, subunit 2 (beta)
1420888_at	0.66	0.73	0.70	0.000411053	12048	Bcl2l1	BCL2-like 1
1416529_at	0.76	0.63	0.70	1.75E-05	13730	Emp1	epithelial membrane protein 1
1448686_at	1.03	0.36	0.70	0.025026854	16170	Il16	interleukin 16
1419637_s_at	0.70	0.69	0.69	2.30E-05	67392	4833420G17Rik	RIKEN cDNA 4833420G17 gene
1450476_at	1.16	0.23	0.69	0.033311066	12802	Cnr2	cannabinoid receptor 2 (macrophage)
1436356_at	0.67	0.71	0.69	0.002048699	74480	Samd4	sterile alpha motif domain containing 4
1435476_a_at	0.94	0.44	0.69	0.006348081	14130	Fcgr2b	Fc receptor, IgG, low affinity IIb
1452976_a_at	0.62	0.76	0.69	1.06E-07	65962	Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2
1420887_a_at	1.00	0.38	0.69	0.019516984	12048	Bcl2l1	BCL2-like 1
1440837_at	0.96	0.40	0.68	0.013507708	15002	H2-Ob	histocompatibility 2, O region beta locus
1456307_s_at	0.99	0.37	0.68	0.011587845	11513	Adcy7	adenylate cyclase 7
1424652_at	0.75	0.61	0.68	0.002052896	232146	Eva1a	eva-1 homolog A (C. elegans)
1449773_s_at	0.80	0.56	0.68	0.000680168	17873	Gadd45b	growth arrest and DNA-damage-inducible 45 beta
1449401_at	0.91	0.44	0.68	0.003483886	12262	C1qc	complement component 1, q subcomponent, C chain
1436097_x_at	1.06	0.29	0.67	0.009056199	216445	Arhgap9	Rho GTPase activating protein 9
1449455_at	1.12	0.22	0.67	0.020310732	15162	Hck	hemopoietic cell kinase
1433862_at	1.03	0.31	0.67	0.008680907	105988	Espl1	extra spindle poles-like 1 (S. cerevisiae)
1452367_at	0.58	0.76	0.67	0.039369732	107684	Coro2a	coronin, actin binding protein 2A
1423593_a_at	1.13	0.20	0.67	0.015550277	12978	Csf1r	colony stimulating factor 1 receptor
1435114_at	0.71	0.62	0.67	0.000315933	218973	Wdhd1	WD repeat and HMG-box DNA binding protein 1
1416246_a_at	0.95	0.38	0.67	0.011830695	12721	Coro1a	coronin, actin binding protein 1A
1448249_at	0.41	0.92	0.66	0.006648104	14555	Gpd1	glycerol-3-phosphate dehydrogenase 1 (soluble)
1433678_at	1.00	0.33	0.66	0.009512891	104759	Pld4	phospholipase D family, member 4
1417391_a_at	1.02	0.31	0.66	0.0380316	16170	Il16	interleukin 16
1424546_at	0.57	0.75	0.66	0.001566039	214489	BC003965	cDNA sequence BC003965
1441069_at	0.86	0.46	0.66	0.018897338	332175	Zdhhc23	zinc finger, DHHC domain containing 23
1436171_at	0.91	0.41	0.66	0.018102907	226652	Arhgap30	Rho GTPase activating protein 30
1427368_x_at	0.70	0.61	0.66	9.47E-05	14159	Fes	feline sarcoma oncogene

1426803_at	0.67	0.64	0.65	0.001104089	74213	Rbm26	RNA binding motif protein 26
1426803_at	0.67	0.64	0.65	0.001104089	100502987	Gm17066	predicted gene 17066
1452928_at	0.99	0.32	0.65	0.005341131	66610	Abi3	ABI gene family, member 3
1427007_at	1.02	0.29	0.65	0.022931094	74131	Sash3	SAM and SH3 domain containing 3
1449127_at	0.98	0.33	0.65	0.004184761	20345	Selplg	selectin, platelet (p-selectin) ligand
1451224_at	1.04	0.26	0.65	0.017396166	56807	Scamp5	secretory carrier membrane protein 5
1417702_a_at	0.85	0.44	0.65	0.008011645	140483	Hnmt	histamine N-methyltransferase
1437635_at	0.65	0.65	0.65	0.008182446	73379	Dcbld2	discoidin, CUB and LCCL domain containing 2
1437635_at	0.65	0.65	0.65	0.008182446	54613	St3gal6	ST3 beta-galactoside alpha-2,3-sialyltransferase 6
1460387_a_at	0.90	0.39	0.65	0.001565101	22619	Siae	sialic acid acetylesterase
1417063_at	0.88	0.42	0.65	0.002850071	12260	C1qb	complement component 1, q subcomponent, beta polypeptide
1454628_at	0.81	0.48	0.65	0.007656163	320678	Iffo1	intermediate filament family orphan 1
1456772_at	0.98	0.31	0.64	0.010381765	17969	Ncf1	neutrophil cytosolic factor 1
1416432_at	0.67	0.62	0.64	0.012895032	170768	Pfkfb3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3
1436088_at	0.80	0.49	0.64	0.006809548	223601	Fam49b	family with sequence similarity 49, member B
1428700_at	0.99	0.29	0.64	0.016942097	74191	P2ry13	purinergic receptor P2Y, G-protein coupled 13
1441799_at	0.88	0.40	0.64	0.0228537	402765	6030422H21Rik	RIKEN cDNA 6030422H21 gene
1433398_at	0.98	0.30	0.64	0.00096958	30938	Fgd3	FYVE, RhoGEF and PH domain containing 3
1430201_at	0.47	0.80	0.64	0.005148103	72804	9130017K11Rik	RIKEN cDNA 9130017K11 gene
1421817_at	0.61	0.65	0.63	0.006548341	14782	Gsr	glutathione reductase
1448123_s_at	0.66	0.61	0.63	0.001480837	21810	Tgfbi	transforming growth factor, beta induced
1450792_at	0.88	0.38	0.63	0.005635757	22177	Tyrobp	TYRO protein tyrosine kinase binding protein
1435375_at	1.06	0.19	0.63	0.012999763	223433	Fam105a	family with sequence similarity 105, member A
1441938_x_at	0.67	0.59	0.63	0.008359043	63955	Cables1	CDK5 and Abl enzyme substrate 1
1434121_at	0.80	0.46	0.63	0.019646145	243914	Lgi4	leucine-rich repeat LGI family, member 4
1450241_a_at	0.93	0.33	0.63	0.037569768	14017	Evi2a	ecotropic viral integration site 2a
1425382_a_at	0.42	0.83	0.63	0.033827645	11829	Aqp4	aquaporin 4
1451655_at	0.89	0.36	0.62	0.014096719	276950	Slfn8	schlafen 8
1434510_at	0.56	0.69	0.62	5.14E-05	23972	Papss2	3'-phosphoadenosine 5'-phosphosulfate synthase 2
1423119_at	0.57	0.67	0.62	3.76E-06	100037282	Rsph3b	radial spoke 3B homolog (Chlamydomonas)
1423119_at	0.57	0.67	0.62	3.76E-06	66832	Rsph3a	radial spoke 3A homolog (Chlamydomonas)
1416882_at	0.92	0.32	0.62	0.009519318	67865	Rgs10	regulator of G-protein signalling 10
1442959_at	0.48	0.76	0.62	0.006317021	12211	Birc6	baculoviral IAP repeat-containing 6
1420630_at	0.75	0.49	0.62	0.000987894	74525	8430419L09Rik	RIKEN cDNA 8430419L09 gene
1456014_s_at	0.85	0.39	0.62	0.006182157	107328	Trpt1	tRNA phosphotransferase 1
1456014_s_at	0.85	0.39	0.62	0.006182157	108101	Fermt3	fermitin family homolog 3 (Drosophila)
1436131_at	0.94	0.30	0.62	0.013935373	233274	Siglech	sialic acid binding Ig-like lectin H
1448407_at	1.05	0.19	0.62	0.013224888	74048	4632428N05Rik	RIKEN cDNA 4632428N05 gene
1436312_at	0.96	0.27	0.62	0.006766225	22778	Ikzf1	IKAROS family zinc finger 1
1434010_at	0.59	0.64	0.62	0.002004467	72750	Fam117b	family with sequence similarity 117, member B
1460656_a_at	0.67	0.56	0.62	0.000526102	106489	Sft2d1	SFT2 domain containing 1
1424400_a_at	0.76	0.47	0.61	0.008651563	107747	Aldh1l1	aldehyde dehydrogenase 1 family, member L1
1460003_at	0.99	0.23	0.61	0.013396838	99132	AI956758	expressed sequence AI956758
1421408_at	1.14	0.08	0.61	0.045116016	80719	Igsf6	immunoglobulin superfamily, member 6
1458351_s_at	0.52	0.71	0.61	0.005303087	77113	Klhl2	kelch-like 2, Mayven
1417590_at	1.07	0.16	0.61	0.011328306	104086	Cyp27a1	cytochrome P450, family 27, subfamily a, polypeptide 1
1438667_at	0.62	0.60	0.61	0.006533232	319613	Sybu	syntabulin (syntaxin-interacting)
1459885_s_at	0.62	0.60	0.61	0.014001037	12867	Cox7c	cytochrome c oxidase subunit VIIc
1459885_s_at	0.62	0.60	0.61	0.014001037	100048613	LOC100048613	cytochrome c oxidase subunit 7C, mitochondrial-like
1435397_at	0.56	0.66	0.61	6.94E-06	235132	Zbtb44	zinc finger and BTB domain containing 44
1455450_at	0.52	0.70	0.61	0.035948152	545622	Ptpn3	protein tyrosine phosphatase, non-receptor type 3
1449130_at	1.01	0.20	0.61	0.007564364	12479	Cd1d1	CD1d1 antigen
1452292_at	1.05	0.16	0.61	0.031491106	71770	Ap2b1	adaptor-related protein complex 2, beta 1 subunit
1435490_at	0.96	0.26	0.61	0.034710901	212032	Hk3	hexokinase 3
1451767_at	1.01	0.20	0.61	0.043371802	17969	Ncf1	neutrophil cytosolic factor 1
1453367_a_at	0.96	0.25	0.61	0.008301366	76192	Abhd12	abhydrolase domain containing 12
1418096_at	0.95	0.26	0.61	0.021894003	27261	Dok3	docking protein 3
1437302_at	0.96	0.25	0.60	0.00572308	11555	Adrb2	adrenergic receptor, beta 2
1425853_s_at	0.73	0.47	0.60	0.033003791	19116	Prlr	prolactin receptor
1419173_at	0.73	0.47	0.60	0.001461794	109652	Acy1	aminoacylase 1
1454764_s_at	0.65	0.56	0.60	0.001097397	105727	Slc38a1	solute carrier family 38, member 1
1436507_at	0.62	0.57	0.60	0.007243588	108960	Irak2	interleukin-1 receptor-associated kinase 2
1416985_at	1.03	0.17	0.60	0.03039922	19261	Sirpa	signal-regulatory protein alpha
1435203_at	0.82	0.37	0.60	0.001006222	140481	Man2a2	mannosidase 2, alpha 2
1418340_at	0.89	0.30	0.59	0.014393622	14127	Fcer1g	Fc receptor, IgE, high affinity I, gamma polypeptide
1421928_at	0.80	0.38	0.59	0.019538078	13838	Epha4	Eph receptor A4
1459971_at	0.35	0.83	0.59	0.003413227	240776	Kcnt2	potassium channel, subfamily T, member 2
1453195_at	0.66	0.52	0.59	0.018349626	68112	Sdccag3	serologically defined colon cancer antigen 3
1453195_at	0.66	0.52	0.59	0.018349626	77276	9430022A06Rik	RIKEN cDNA 9430022A06 gene
1442082_at	0.91	0.26	0.59	0.040160642	12267	C3ar1	complement component 3a receptor 1
1434225_at	0.51	0.67	0.59	3.06E-05	20947	Swap70	SWA-70 protein
1436574_at	0.65	0.52	0.59	2.40E-05	70005	Znf41-ps	ZNF41, pseudogene
1417928_at	0.64	0.53	0.58	0.021333145	30794	Pdlim4	PDZ and LIM domain 4
1452604_at	0.57	0.60	0.58	0.001946418	243362	Stard13	StAR-related lipid transfer (START) domain containing 13
1416805_at	0.49	0.68	0.58	0.000817646	68659	Fam198b	family with sequence similarity 198, member B
1416135_at	0.61	0.55	0.58	0.010005122	11792	Apex1	apurinic/apyrimidinic endonuclease 1
1419515_at	0.93	0.24	0.58	0.023717682	26382	Fgd2	FYVE, RhoGEF and PH domain containing 2

1445667_at	0.58	0.58	0.58	0.002502234	103724	Tbc1d10a	TBC1 domain family, member 10a
1455015_at	0.73	0.43	0.58	0.018258318	71310	Tbc1d9	TBC1 domain family, member 9
1426615_s_at	0.49	0.67	0.58	0.007064096	234593	Ndrg4	N-myc downstream regulated gene 4
1440285_at	0.74	0.42	0.58	0.00089513	243725	Ppp1r9a	protein phosphatase 1, regulatory (inhibitor) subunit 9A
1455885_at	0.72	0.43	0.58	0.048357892	231842	Amz1	archaelysin family metallopeptidase 1
1426852_x_at	0.45	0.71	0.58	0.008497043	18133	Nov	nephroblastoma overexpressed gene
1427892_at	0.87	0.28	0.58	0.03271002	246177	Myo1g	myosin IG
1432517_a_at	0.44	0.71	0.57	0.002739798	18113	Nnmt	nicotinamide N-methyltransferase
1437913_at	0.08	1.06	0.57	0.011959451	12047	Bcl2a1d	B cell leukemia/lymphoma 2 related protein A1d
1437913_at	0.08	1.06	0.57	0.011959451	12044	Bcl2a1a	B cell leukemia/lymphoma 2 related protein A1a
1437913_at	0.08	1.06	0.57	0.011959451	12045	Bcl2a1b	B cell leukemia/lymphoma 2 related protein A1b
1417779_at	0.81	0.33	0.57	0.006997443	66566	Ntpcr	nucleoside-triphosphatase, cancer-related
1455056_at	0.54	0.60	0.57	2.12E-05	380928	Lmo7	LIM domain only 7
1460206_at	0.47	0.67	0.57	0.003980863	56149	Grasp	GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein
1424784_at	0.62	0.52	0.57	0.000438721	70005	Znf41-ps	ZNF41, pseudogene
1424784_at	0.62	0.52	0.57	0.000438721	666532	Gm13139	predicted gene 13139
1424784_at	0.62	0.52	0.57	0.000438721	100503000	Gm13248	predicted gene 13248
1424784_at	0.62	0.52	0.57	0.000438721	210853	Zfp947	zinc finger protein 947
1424784_at	0.62	0.52	0.57	0.000438721	433791	Gm13251	predicted gene 13251
1437356_at	0.85	0.29	0.57	0.027318781	321019	Gpr183	G protein-coupled receptor 183
1454974_at	0.46	0.67	0.57	0.036643268	18208	Ntn1	netrin 1
1425094_a_at	0.52	0.62	0.57	0.002912718	16874	Lhx6	LIM homeobox protein 6
1415842_at	0.48	0.66	0.57	7.59E-05	56716	Mlst8	MTOR associated protein, LST8 homolog (S. cerevisiae)
1453839_a_at	0.66	0.47	0.57	0.008276174	74116	Pi16	peptidase inhibitor 16
1428954_at	0.50	0.63	0.57	1.47E-07	65962	Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2
1422755_at	1.05	0.08	0.57	0.026399335	12229	Btk	Bruton agammaglobulinemia tyrosine kinase
1456072_at	0.71	0.42	0.56	0.000254011	243725	Ppp1r9a	protein phosphatase 1, regulatory (inhibitor) subunit 9A
1420955_at	0.32	0.80	0.56	0.033223077	26950	Vsnl1	visinin-like 1
1423768_at	0.81	0.32	0.56	0.003247903	54445	Unc93b1	unc-93 homolog B1 (C. elegans)
1440878_at	1.00	0.13	0.56	0.036784598	12394	Runx1	runt related transcription factor 1
1453768_a_at	0.66	0.46	0.56	5.48E-06	73847	Fam110a	family with sequence similarity 110, member A
1451161_a_at	0.97	0.16	0.56	0.031016454	13733	Emr1	EGF-like module containing, mucin-like, hormone receptor-like sequence 1
1426851_a_at	0.39	0.72	0.56	0.008348861	18133	Nov	nephroblastoma overexpressed gene
1431208_a_at	0.41	0.71	0.56	0.000119205	65962	Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2
1436781_at	0.79	0.32	0.56	0.033329173	17159	Man2b1	mannosidase 2, alpha B1
1415698_at	0.72	0.39	0.56	0.000405403	105348	Golm1	golgi membrane protein 1
1450234_at	0.75	0.36	0.56	0.023798903	73656	Ms4a6c	membrane-spanning 4-domains, subfamily A, member 6C
1455269_a_at	0.77	0.34	0.55	0.036582641	12721	Coro1a	coronin, actin binding protein 1A
1424732_s_at	0.52	0.59	0.55	0.000515949	73067	Tmem192	transmembrane protein 192
1435113_x_at	0.30	0.81	0.55	0.027318117	20262	Stmn3	stathmin-like 3
1436576_at	1.09	0.01	0.55	0.0416076	215900	Fam26f	family with sequence similarity 26, member F
1428397_at	0.96	0.15	0.55	0.015699263	93961	B3galt5	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5
1422638_s_at	0.88	0.22	0.55	0.014827966	54354	Rassf5	Ras association (RalGDS/AF-6) domain family member 5
1439966_x_at	0.63	0.47	0.55	0.022250589	94279	Sfxn2	sideroflexin 2
1419465_at	0.33	0.76	0.55	0.005566602	72293	Nkd2	naked cuticle 2 homolog (Drosophila)
1439947_at	0.46	0.63	0.55	0.00631631	13070	Cyp11a1	cytochrome P450, family 11, subfamily a, polypeptide 1
1419662_at	0.36	0.73	0.55	0.005804911	18295	Ogn	osteoglycin
1418163_at	1.01	0.08	0.55	0.023884028	21898	Tlr4	toll-like receptor 4
1418110_a_at	0.79	0.31	0.55	0.003955956	16331	Inpp5d	inositol polyphosphate-5-phosphatase D
1418252_at	0.91	0.18	0.55	0.005007501	18600	Padi2	peptidyl arginine deiminase, type II
1429122_a_at	0.47	0.63	0.55	0.000123696	73327	Pradc1	protease-associated domain containing 1
1418261_at	0.99	0.10	0.55	0.040998678	20963	Syk	spleen tyrosine kinase
1428955_x_at	0.51	0.58	0.55	1.07E-08	65962	Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2
1455695_at	0.51	0.58	0.54	0.000533867	20449	St8sia1	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1
1440813_s_at	0.86	0.23	0.54	0.005478529	140571	Plxnb3	plexin B3
1441890_x_at	0.42	0.66	0.54	0.035932906	230157	Tmeff1	transmembrane protein with EGF-like and two follistatin-like domains 1
1417750_a_at	0.72	0.36	0.54	0.000794219	67712	Slc25a37	solute carrier family 25, member 37
1436684_a_at	0.49	0.59	0.54	4.24E-05	67045	Riok2	RIO kinase 2 (yeast)
1439500_at	0.47	0.60	0.54	3.28E-05	69938	Scrn1	secernin 1
1426794_at	0.63	0.43	0.53	0.000496244	19280	Ptprs	protein tyrosine phosphatase, receptor type, S
1416773_at	0.42	0.64	0.53	0.021348728	22390	Wee1	WEE 1 homolog 1 (S. pombe)
1439895_at	0.61	0.45	0.53	0.00654799	105285	AU021025	expressed sequence AU021025
1455345_at	0.60	0.46	0.53	0.002133825	76901	Phf15	PHD finger protein 15
1422124_a_at	0.83	0.23	0.53	0.03681439	19264	Ptprc	protein tyrosine phosphatase, receptor type, C
1442740_at	0.68	0.38	0.53	0.006704834	70779	Prdm5	PR domain containing 5
1433587_at	0.59	0.47	0.53	0.000387068	68799	Rgmb	RGM domain family, member B
1452847_at	0.47	0.59	0.53	0.005052217	71962	Gatsl3	GATS protein-like 3
1420703_at	0.69	0.37	0.53	0.022710448	12982	Csf2ra	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)
1438434_at	0.64	0.42	0.53	0.014126269	228482	Arhgap11a	Rho GTPase activating protein 11A
1451461_a_at	0.40	0.66	0.53	0.011497805	11676	Aldoc	aldolase C, fructose-bisphosphate
1434202_a_at	0.43	0.63	0.53	0.001025013	268709	Fam107a	family with sequence similarity 107, member A
1451353_at	0.59	0.46	0.53	0.000465179	107769	Tm6sf1	transmembrane 6 superfamily member 1
1436448_a_at	0.89	0.17	0.53	0.020901825	19224	Ptgs1	prostaglandin-endoperoxide synthase 1
1419663_at	0.39	0.66	0.53	0.000169098	18295	Ogn	osteoglycin
1441823_at	0.32	0.73	0.52	0.049774861	328365	Zmiz1	zinc finger, MIZ-type containing 1
1448620_at	0.84	0.21	0.52	0.013046007	14131	Fcgr3	Fc receptor, IgG, low affinity III
1448885_at	0.59	0.45	0.52	0.018139353	74012	Rap2b	RAP2B, member of RAS oncogene family

1455649_at	0.84	0.20	0.52	0.004798539	69480	Ttc9	tetratricopeptide repeat domain 9
1451924_a_at	0.62	0.43	0.52	0.013992849	13614	Edn1	endothelin 1
1420818_at	1.02	0.02	0.52	0.04248638	20491	Sla	src-like adaptor
1435342_at	0.83	0.21	0.52	0.007071287	52150	Kcnk6	potassium inwardly-rectifying channel, subfamily K, member 6
1431805_a_at	0.42	0.61	0.52	0.002004122	52428	Rhpn2	rhophilin, Rho GTPase binding protein 2
1436545_at	0.92	0.12	0.52	0.039914843	207521	Dtx4	deltex 4 homolog (Drosophila)
1436188_a_at	0.43	0.61	0.52	0.012787156	234593	Ndrg4	N-myc downstream regulated gene 4
1460251_at	0.36	0.67	0.51	0.010652442	14102	Fas	Fas (TNF receptor superfamily member 6)
1417545_at	0.77	0.25	0.51	0.036522374	63873	Trpv4	transient receptor potential cation channel, subfamily V, member 4
1423364_a_at	0.62	0.40	0.51	0.034523199	14339	Aktip	thymoma viral proto-oncogene 1 interacting protein
1452661_at	0.40	0.61	0.51	0.000692329	22042	Tfrc	transferrin receptor
1433694_at	0.84	0.17	0.51	0.019165134	18576	Pde3b	phosphodiesterase 3B, cGMP-inhibited
1447849_s_at	0.76	0.25	0.50	0.012644061	17132	Maf	avian musculoaponeurotic fibrosarcoma (v-maf) AS42 oncogene homolog
1452410_a_at	0.59	0.42	0.50	0.000117003	14159	Fes	feline sarcoma oncogene
1426657_s_at	0.70	0.31	0.50	0.009638493	666422	Gm8096	3-phosphoglycerate dehydrogenase pseudogene
1426657_s_at	0.70	0.31	0.50	0.009638493	236539	Phgdh	3-phosphoglycerate dehydrogenase
1419466_at	0.39	0.61	0.50	0.02436671	72293	Nkd2	naked cuticle 2 homolog (Drosophila)
1440999_at	0.63	0.37	0.50	0.01736297	242109	Zfp697	zinc finger protein 697
1452893_s_at	0.32	0.68	0.50	0.024476839	69638	Enho	energy homeostasis associated
1422864_at	0.77	0.23	0.50	0.017181631	12394	Runx1	runt related transcription factor 1
1427004_at	0.24	0.75	0.50	0.018817063	230904	Fbxo2	F-box protein 2
1429175_at	0.40	0.60	0.50	0.002070458	68027	Tmem178	transmembrane protein 178
1433939_at	0.37	0.62	0.50	0.001941468	16764	Aff3	AF4/FMR2 family, member 3
1426450_at	0.79	0.20	0.50	0.046458127	224860	Plcl2	phospholipase C-like 2
1429298_at	0.17	0.82	0.49	0.028227057	69219	Ddah1	dimethylarginine dimethylaminohydrolase 1
1448328_at	0.77	0.22	0.49	0.037834794	24055	Sh3bp2	SH3-domain binding protein 2
1454995_at	0.38	0.60	0.49	0.002248943	69219	Ddah1	dimethylarginine dimethylaminohydrolase 1
1416666_at	0.61	0.37	0.49	0.000662116	20720	Serpine2	serine (or cysteine) peptidase inhibitor, clade E, member 2
1438511_a_at	0.35	0.63	0.49	0.016377543	66214	Rgcc	regulator of cell cycle
1448748_at	0.70	0.28	0.49	0.040387273	56193	Plek	pleckstrin
1426658_x_at	0.65	0.33	0.49	0.007113573	236539	Phgdh	3-phosphoglycerate dehydrogenase
1449453_at	0.72	0.26	0.49	0.03160366	12182	Bst1	bone marrow stromal cell antigen 1
1434265_s_at	0.24	0.73	0.49	0.007222363	109676	Ank2	ankyrin 2, brain
1428222_at	0.60	0.37	0.49	0.000281948	70762	Dclk2	doublecortin-like kinase 2
1422603_at	0.62	0.35	0.49	0.000261366	58809	Rnase4	ribonuclease, RNase A family 4
1449282_at	0.70	0.27	0.49	0.03065623	58861	Cysltr1	cysteinyl leukotriene receptor 1
1425609_at	0.81	0.16	0.49	0.044785835	17969	Ncf1	neutrophil cytosolic factor 1
1448167_at	0.72	0.25	0.48	0.001160993	15979	Ifngr1	interferon gamma receptor 1
1421937_at	0.78	0.18	0.48	0.024451153	26377	Dapp1	dual adaptor for phosphotyrosine and 3-phosphoinositides 1
1447901_x_at	0.32	0.64	0.48	0.001035877	78887	Sfi1	Sfi1 homolog, spindle assembly associated (yeast)
1447901_x_at	0.32	0.64	0.48	0.001035877	100861749	LOC100861749	protein SFI1 homolog
1447901_x_at	0.32	0.64	0.48	0.001035877	66776	Pisd-ps3	phosphatidylserine decarboxylase, pseudogene 3
1416795_at	0.71	0.25	0.48	0.003669538	68631	Cryl1	crystallin, lambda 1
1435582_at	0.74	0.21	0.48	0.02227104	545030	Wdfy4	WD repeat and FYVE domain containing 4
1417669_at	0.70	0.25	0.48	0.003801843	76192	Abhd12	abhydrolase domain containing 12
1452117_a_at	0.66	0.29	0.47	0.029797571	23880	Fyb	FYN binding protein
1428429_at	0.68	0.26	0.47	0.007061708	68799	Rgmb	RGM domain family, member B
1439860_at	0.59	0.35	0.47	0.00461763	13631	Eef2k	eukaryotic elongation factor-2 kinase
1425282_at	0.28	0.66	0.47	0.009205325	218215	Rnf144b	ring finger protein 144B
1420836_at	0.65	0.30	0.47	0.002544175	67554	Slc25a30	solute carrier family 25, member 30
1453286_at	0.32	0.62	0.47	0.012199658	18845	Plxna2	plexin A2
1429761_at	0.78	0.16	0.47	0.012814936	104001	Rtn1	reticulon 1
1457829_at	0.84	0.09	0.47	0.04156597	12745	Clgn	calmegin
1416361_a_at	0.35	0.58	0.47	0.002770992	13426	Dync1i1	dynein cytoplasmic 1 intermediate chain 1
1434559_at	0.32	0.61	0.46	0.003287208	20908	Stx3	syntaxin 3
1453135_at	0.16	0.77	0.46	0.025081651	384061	Fndc5	fibronectin type III domain containing 5
1450097_s_at	0.71	0.21	0.46	0.043251667	14673	Gna12	guanine nucleotide binding protein, alpha 12
1434653_at	0.73	0.19	0.46	0.006408334	19229	Ptk2b	PTK2 protein tyrosine kinase 2 beta
1423655_a_at	0.77	0.16	0.46	0.012498119	68964	Ctc1	CTS telomere maintenance complex component 1
1416619_at	0.77	0.15	0.46	0.023010929	74048	4632428N05Rik	RIKEN cDNA 4632428N05 gene
1435975_at	0.66	0.26	0.46	0.002236248	102442	Dennd4a	DENN/MADD domain containing 4A
1417654_at	0.61	0.29	0.45	0.026194022	20971	Sdc4	syndecan 4
1445246_at	0.64	0.26	0.45	0.029884603	320806	Gfm2	G elongation factor, mitochondrial 2
1422973_a_at	0.31	0.59	0.45	0.003769097	21835	Thrsp	thyroid hormone responsive
1437419_at	0.61	0.29	0.45	0.008633001	140780	Bmp2k	BMP2 inducible kinase
1442903_at	0.59	0.30	0.45	0.022416597	106967	4732423E21Rik	RIKEN cDNA 4732423E21 gene
1417268_at	0.73	0.16	0.45	0.046199729	12475	Cd14	CD14 antigen
1457454_at	0.25	0.64	0.44	0.012722617	74996	Usp47	ubiquitin specific peptidase 47
1457454_at	0.25	0.64	0.44	0.012722617	52400	D7Ertd602e	DNA segment, Chr 7, ERATO Doi 602, expressed
1441652_at	0.26	0.63	0.44	0.003671493	12168	Bmpr2	bone morphogenetic protein receptor, type II (serine/threonine kinase)
1448139_at	0.24	0.65	0.44	0.046934423	170790	Mlc1	megalencephalic leukoencephalopathy with subcortical cysts 1 homolog (human)
1425598_a_at	0.74	0.15	0.44	0.022777346	17096	Lyn	Yamaguchi sarcoma viral (v-yes-1) oncogene homolog
1425598_a_at	0.74	0.15	0.44	0.022777346	666513	Gm11787	predicted gene 11787
1456716_s_at	0.30	0.58	0.44	0.024910432	76482	3110002H16Rik	RIKEN cDNA 3110002H16 gene
1417611_at	0.59	0.29	0.44	0.001549582	170706	Tmem37	transmembrane protein 37
1434028_at	0.19	0.69	0.44	0.006760495	11864	Arnt2	aryl hydrocarbon receptor nuclear translocator 2
1429583_at	0.29	0.59	0.44	0.006155635	100503890	Pet100	PET100 homolog (S. cerevisiae)

1418638_at	0.72	0.15	0.44	0.010526837	14999	H2-DMb1	histocompatibility 2, class II, locus Mb1
1418638_at	0.72	0.15	0.44	0.010526837	15000	H2-DMb2	histocompatibility 2, class II, locus Mb2
1453294_at	0.22	0.66	0.44	0.048798072	74173	1700012B15Rik	RIKEN cDNA 1700012B15 gene
1456060_at	0.59	0.28	0.44	0.004473721	17132	Maf	avian musculoaponeurotic fibrosarcoma (v-maf) AS42 oncogene homolog
1447112_s_at	0.64	0.23	0.43	0.009468335	68631	Cryl1	crystallin, lambda 1
1425311_at	0.67	0.20	0.43	0.007183833	78792	4930432F04Rik	RIKEN cDNA 4930432F04 gene
1455671_at	0.63	0.23	0.43	0.000513843	27784	Commd8	COMM domain containing 8
1422656_at	0.69	0.17	0.43	0.012952506	19428	Rasl2-9	RAS-like, family 2, locus 9
1421936_at	0.76	0.09	0.43	0.044443256	26377	Dapp1	dual adaptor for phosphotyrosine and 3-phosphoinositides 1
1439902_at	0.83	0.02	0.42	0.043812663	12273	C5ar1	complement component 5a receptor 1
1456153_at	0.66	0.19	0.42	0.003883071	237860	Ssh2	slingshot homolog 2 (Drosophila)
1416762_at	0.18	0.66	0.42	0.010234523	20194	S100a10	S100 calcium binding protein A10 (calpactin)
1419248_at	0.72	0.12	0.42	0.046650945	19735	Rgs2	regulator of G-protein signaling 2
1428156_at	0.63	0.20	0.42	0.014871234	14702	Gng2	guanine nucleotide binding protein (G protein), gamma 2
1456069_at	0.22	0.61	0.42	0.025060983	13527	Dtna	dystrobrevin alpha
1448364_at	0.64	0.19	0.42	0.008467734	12452	Ccng2	cyclin G2
1435642_at	0.61	0.21	0.41	0.017790634	320111	Prr18	proline rich region 18
1447813_x_at	0.71	0.11	0.41	0.022066399	20491	Sla	src-like adaptor
1428758_at	0.74	0.07	0.41	0.043645266	67893	Tmem86a	transmembrane protein 86A
1420895_at	0.64	0.17	0.41	0.009948321	21812	Tgfbr1	transforming growth factor, beta receptor I
1426239_s_at	0.62	0.19	0.40	0.045031469	216869	Arrb2	arrestin, beta 2
1436610_at	0.20	0.59	0.40	0.038191699	106585	Ankrd12	ankyrin repeat domain 12
1423656_x_at	0.68	0.10	0.39	0.019177409	68964	Ctc1	CTS telomere maintenance complex component 1
1451019_at	0.58	0.20	0.39	0.003066548	56464	Ctsf	cathepsin F
1447063_at	0.75	0.03	0.39	0.02243133	74211	1700017B05Rik	RIKEN cDNA 1700017B05 gene
1449640_at	0.67	0.10	0.39	0.039403683	170743	Tlr7	toll-like receptor 7
1448021_at	0.74	0.03	0.39	0.029246669	74645	Fam46c	family with sequence similarity 46, member C
1424459_at	0.62	0.15	0.38	0.014866156	210992	Lpcat1	lysophosphatidylcholine acyltransferase 1
1460425_at	0.60	0.16	0.38	0.013822046	75462	1700001C19Rik	RIKEN cDNA 1700001C19 gene
1436764_at	0.16	0.59	0.38	0.008768927	93742	Pard3	par-3 (partitioning defective 3) homolog (C. elegans)
1419873_s_at	0.63	0.12	0.37	0.036585307	12978	Csf1r	colony stimulating factor 1 receptor
1438431_at	0.66	0.08	0.37	0.037015525	26874	Abcd2	ATP-binding cassette, sub-family D (ALD), member 2
1423695_at	0.59	0.15	0.37	0.013937785	108687	Edem2	ER degradation enhancer, mannosidase alpha-like 2
1429104_at	0.58	0.15	0.37	0.045519404	632329	LOC632329	LIM domain-containing protein 2-like
1429104_at	0.58	0.15	0.37	0.045519404	67803	Limd2	LIM domain containing 2
1439622_at	0.59	0.12	0.36	0.042533039	213391	Rassf4	Ras association (RalGDS/AF-6) domain family member 4
1420905_at	0.72	-0.02	0.35	0.047570409	16172	Il17ra	interleukin 17 receptor A
1454880_s_at	0.63	0.05	0.34	0.013809987	171543	Bmf	BCL2 modifying factor
1419086_at	0.61	0.04	0.32	0.043648438	14181	Fgfbp1	fibroblast growth factor binding protein 1
1454897_at	0.58	0.02	0.30	0.036948868	102913	6330509M05Rik	RIKEN cDNA 6330509M05 gene

Supplemental Table III: Endothelial gene transcripts differentially expressed in *Notch3*$^{-/-}$ vs WT

Affymetrix probe set ID	Cerebrum N3$^{-/-}$ vs WT (log2)	Cerebellum N3$^{-/-}$ vs WT (log2)	Average fold (log2)	P value	ENTREZ ID	Symbol	Gene Name
1422028_a_at	-3.58	-3.80	-3.69	1.15E-09	23871	Ets1	E26 avian leukemia oncogene 1, 5' domain
1446303_at	-1.68	-1.69	-1.68	0.011229188	16001	Igf1r	insulin-like growth factor I receptor
1418517_at	-1.71	-1.64	-1.67	0.000117328	16373	Irx3	Iroquois related homeobox 3 (Drosophila)
1418536_at	-1.57	-1.38	-1.48	0.01467538	68395	LOC68395	histocompatibility 2, Q region locus 6-like
1447863_s_at	-1.26	-1.30	-1.28	0.000100708	18227	Nr4a2	nuclear receptor subfamily 4, group A, member 2
1438031_at	-1.15	-1.20	-1.18	0.003555772	240168	Rasgrp3	RAS, guanyl releasing protein 3
1451644_a_at	-1.14	-1.13	-1.14	0.039093044	110557	H2-Q6	histocompatibility 2, Q region locus 6
1453855_at	-1.24	-0.90	-1.07	7.18E-06	67622	Mxra7	matrix-remodelling associated 7
1416505_at	-1.42	-0.68	-1.05	0.005256069	15370	Nr4a1	nuclear receptor subfamily 4, group A, member 1
1437247_at	-0.97	-1.01	-0.99	7.59E-05	14284	Fosl2	fos-like antigen 2
1456793_at	-0.83	-1.11	-0.97	0.001410625	231162	Cytl1	cytokine-like 1
1449363_at	-1.10	-0.80	-0.95	0.000100393	11910	Atf3	activating transcription factor 3
1422631_at	-1.00	-0.88	-0.94	5.20E-05	11622	Ahr	aryl-hydrocarbon receptor
1421826_at	-0.92	-0.93	-0.92	0.006284777	54485	Dll4	delta-like 4 (Drosophila)
1436329_at	-1.36	-0.47	-0.92	0.036972206	13655	Egr3	early growth response 3
1423319_at	-0.83	-1.00	-0.92	0.0055513	15242	Hhex	hematopoietically expressed homeobox
1422134_at	-0.21	-1.57	-0.89	0.025705423	14282	Fosb	FBJ osteosarcoma oncogene B
1422882_at	-0.80	-0.97	-0.89	0.000447855	19027	Sypl	synaptophysin-like protein
1422905_s_at	-0.99	-0.78	-0.88	0.000490996	55990	Fmo2	flavin containing monooxygenase 2
1451340_at	-1.08	-0.66	-0.87	0.002066606	214855	Arid5a	AT rich interactive domain 5A (MRF1-like)
1418280_at	-1.17	-0.57	-0.87	0.004021234	23849	Klf6	Kruppel-like factor 6
1437928_at	-1.17	-0.55	-0.86	0.026204492	53601	Pcdh12	protocadherin 12
1448325_at	-0.88	-0.81	-0.84	5.39E-05	17872	Ppp1r15a	protein phosphatase 1, regulatory (inhibitor) subunit 15A
1456874_at	-0.78	-0.89	-0.84	0.00027304	399558	Flrt2	fibronectin leucine rich transmembrane protein 2
1416039_x_at	-1.00	-0.67	-0.83	0.003173488	16007	Cyr61	cysteine rich protein 61
1435137_s_at	-0.92	-0.70	-0.81	9.51E-06	319269	A130040M12Rik	RIKEN cDNA A130040M12 gene
1435137_s_at	-0.92	-0.70	-0.81	9.51E-06	71739	1200015M12Rik	RIKEN cDNA 1200015M12 gene
1449311_at	-0.70	-0.88	-0.79	0.000106017	12013	Bach1	BTB and CNC homology 1
1457404_at	-0.84	-0.70	-0.77	0.001113197	80859	Nfkbiz	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, zeta
1451475_at	-0.86	-0.60	-0.73	0.025655442	67784	Plxnd1	plexin D1
1431833_a_at	-0.75	-0.69	-0.72	0.033968078	15360	Hmgcs2	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2
1439794_at	-0.74	-0.69	-0.72	2.07E-06	57764	Ntn4	netrin 4
1456446_at	-0.73	-0.70	-0.71	0.026595192	67647	4930523C07Rik	RIKEN cDNA 4930523C07 gene
1450051_at	-0.47	-0.93	-0.70	0.00745255	22589	Atrx	alpha thalassemia/mental retardation syndrome X-linked homolog (human)
1423141_at	-0.90	-0.49	-0.69	0.004330725	16889	Lipa	lysosomal acid lipase A
1422642_at	-0.83	-0.55	-0.69	2.26E-05	260409	Cdc42ep3	CDC42 effector protein (Rho GTPase binding) 3
1419209_at	-0.93	-0.43	-0.68	0.013153828	14825	Cxcl1	chemokine (C-X-C motif) ligand 1
1440346_at	-0.63	-0.72	-0.67	0.00565103	216850	Kdm6b	KDM1 lysine (K)-specific demethylase 6B
1460465_at	-0.79	-0.53	-0.66	0.004072655	68169	Ndnf	neuron-derived neurotrophic factor
1417022_at	-0.77	-0.53	-0.65	0.042741285	11989	Slc7a3	solute carrier family 7 (cationic amino acid transporter, y+ system), member 3
1455836_at	-0.45	-0.84	-0.64	0.007672541	18789	Papola	poly (A) polymerase alpha
1434441_at	-0.62	-0.64	-0.63	0.005334421	66129	Aaed1	AhpC/TSA antioxidant enzyme domain containing 1
1437734_at	-0.59	-0.66	-0.62	1.66E-05	17931	Ppp1r12a	protein phosphatase 1, regulatory (inhibitor) subunit 12A
1450716_at	-0.64	-0.58	-0.61	0.010022105	11504	Adamts1	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 1
1419697_at	-0.71	-0.51	-0.61	2.60E-05	56066	Cxcl11	chemokine (C-X-C motif) ligand 11
1429506_at	-0.74	-0.46	-0.60	0.001020102	93960	Nkd1	naked cuticle 1 homolog (Drosophila)
1439757_s_at	-0.63	-0.56	-0.59	9.81E-07	13838	Epha4	Eph receptor A4
1424504_at	-0.55	-0.63	-0.59	0.000357845	19334	Rab22a	RAB22A, member RAS oncogene family
1447100_s_at	-0.62	-0.54	-0.58	1.01E-06	70617	5730508B09Rik	RIKEN cDNA 5730508B09 gene
1425156_at	-0.48	-0.68	-0.58	0.007305022	229900	Gbp7	guanylate binding protein 7
1426914_at	-0.55	-0.60	-0.58	0.013230918	218518	Marveld2	MARVEL (membrane-associating) domain containing 2
1435029_at	-0.48	-0.66	-0.57	3.47E-05	65964	B230120H23Rik	RIKEN cDNA B230120H23 gene
1437057_at	-0.67	-0.45	-0.56	0.003606466	230971	Megf6	multiple EGF-like-domains 6
1447685_x_at	-0.52	-0.60	-0.56	0.00551794	23872	Ets2	E26 avian leukemia oncogene 2, 3' domain
1419639_at	-0.59	-0.52	-0.56	0.001258957	13642	Efnb2	ephrin B2
1422805_a_at	-0.66	-0.43	-0.55	0.001961921	71777	Ing3	inhibitor of growth family, member 3
1423201_at	-0.51	-0.59	-0.55	0.000693936	20185	Ncor1	nuclear receptor co-repressor 1
1436172_at	-0.60	-0.43	-0.51	4.82E-05	330256	Gm20559	predicted gene, 20559
1418289_at	-0.61	-0.37	-0.49	0.000196724	18008	Nes	nestin
1417395_at	-0.58	-0.39	-0.49	0.001283066	16600	Klf4	Kruppel-like factor 4 (gut)
1419699_at	-0.62	-0.27	-0.44	0.020770004	68662	Scgb3a1	secretoglobin, family 3A, member 1
1436446_at	-0.19	-0.68	-0.43	0.00825176	74177	2310007O11Rik	RIKEN cDNA 2310007O11 gene
1417040_a_at	-0.59	-0.23	-0.41	0.022085282	51800	Bok	BCL2-related ovarian killer protein
1449152_at	-0.60	-0.22	-0.41	0.006292242	12579	Cdkn2b	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)
1456762_at	-0.62	-0.19	-0.41	0.039646586	231931	Gimap6	GTPase, IMAP family member 6
1453286_at	0.32	0.62	0.47	0.012199658	18845	Plxna2	plexin A2
1425282_at	0.28	0.66	0.47	0.009205325	218215	Rnf144b	ring finger protein 144B
1452661_at	0.40	0.61	0.51	0.000692329	22042	Tfrc	transferrin receptor
1460251_at	0.36	0.67	0.51	0.010652442	14102	Fas	Fas (TNF receptor superfamily member 6)
1451924_a_at	0.62	0.43	0.52	0.013992849	13614	Edn1	endothelin 1

1451353_at	0.59	0.46	0.53	0.000465179	107769	Tm6sf1	transmembrane 6 superfamily member 1
1416773_at	0.42	0.64	0.53	0.021348728	22390	Wee1	WEE 1 homolog 1 (S. pombe)
1460206_at	0.47	0.67	0.57	0.003980863	56149	Grasp	GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein
1455056_at	0.54	0.60	0.57	2.12E-05	380928	Lmo7	LIM domain only 7
1416805_at	0.49	0.68	0.58	0.000817646	68659	Fam198b	family with sequence similarity 198, member B
1452604_at	0.57	0.60	0.58	0.001946418	243362	Stard13	StAR-related lipid transfer (START) domain containing 13
1434225_at	0.51	0.67	0.59	3.06E-05	20947	Swap70	SWA-70 protein
1434010_at	0.59	0.64	0.62	0.002004467	72750	Fam117b	family with sequence similarity 117, member B
1452976_a_at	0.62	0.76	0.69	1.06E-07	65962	Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2
1416529_at	0.76	0.63	0.70	1.75E-05	13730	Emp1	epithelial membrane protein 1
1420888_at	0.66	0.73	0.70	0.000411053	12048	Bcl2l1	BCL2-like 1
1429214_at	0.38	1.04	0.71	0.006245632	77794	Adamtsl2	ADAMTS-like 2
1450971_at	0.77	0.65	0.71	0.000429117	17873	Gadd45b	growth arrest and DNA-damage-inducible 45 beta
1428455_at	0.59	0.96	0.78	0.004335871	12818	Col14a1	collagen, type XIV, alpha 1
1417184_s_at	0.34	1.27	0.80	0.046613815	100503605	Beta-s	hemoglobin subunit beta-1-like
1417184_s_at	0.34	1.27	0.80	0.046613815	15129	Hbb-b1	hemoglobin, beta adult major chain
1417184_s_at	0.34	1.27	0.80	0.046613815	15130	Hbb-b2	hemoglobin, beta adult minor chain
1422771_at	0.67	0.94	0.80	0.000779146	17130	Smad6	SMAD family member 6
1435188_at	0.63	1.18	0.90	0.040239345	229599	Gm129	predicted gene 129
1435918_at	0.82	1.03	0.93	0.013077582	268709	Fam107a	family with sequence similarity 107, member A
1435292_at	0.97	0.89	0.93	0.003438294	210789	Tbc1d4	TBC1 domain family, member 4
1451006_at	1.10	1.14	1.12	0.001820219	22436	Xdh	xanthine dehydrogenase
1426464_at	1.23	1.34	1.29	0.046201091	217166	Nr1d1	nuclear receptor subfamily 1, group D, member 1
1418203_at	1.36	1.26	1.31	3.03E-05	58801	Pmaip1	phorbol-12-myristate-13-acetate-induced protein 1
1418003_at	1.01	1.63	1.32	0.000551981	66214	Rgcc	regulator of cell cycle
1426472_at	1.49	1.29	1.39	0.000289519	22710	Zfp52	zinc finger protein 52
1421144_at	4.51	5.05	4.78	5.53E-10	77945	Rpgrip1	retinitis pigmentosa GTPase regulator interacting protein 1

Supplemental Table IV: Pericyte gene transcripts differentially expressed in *Notch3*$^{-/-}$ vs WT

Affymetrix probe set ID	Cerebrum N3 /- vs WT (log2)	Cerebellum N3-/- vs WT (log2)	Average fold (log2)	P value	ENTREZ ID	Symbol	Gene Name
1421965_s_at	-8.55	-8.77	-8.66	2.22E-11	18131	Notch3	notch 3
1422529_s_at	-3.26	-2.51	-2.88	8.14E-08	12373	Casq2	calsequestrin 2
1460458_at	-2.39	-2.55	-2.47	6.13E-07	78892	Crispld2	cysteine-rich secretory protein LCCL domain containing 2
1418156_at	-2.46	-1.98	-2.22	5.25E-08	57814	Kcne4	potassium voltage-gated channel, Isk-related subfamily, gene 4
1422545_at	-1.94	-1.74	-1.84	3.97E-07	21385	Tbx2	T-box 2
1451691_at	-1.76	-1.82	-1.79	5.52E-06	13617	Ednra	endothelin receptor type A
1426571_at	-1.89	-1.57	-1.73	1.99E-06	101772	Ano1	anoctamin 1, calcium activated chloride channel
1420533_at	-1.42	-1.69	-1.56	7.63E-06	60596	Gucy1a3	guanylate cyclase 1, soluble, alpha 3
1455271_at	-1.37	-1.45	-1.41	2.67E-06	620695	Gm13889	predicted gene 13889
1437173_at	-1.36	-1.38	-1.37	4.68E-09	13610	S1pr3	sphingosine-1-phosphate receptor 3
1439172_at	-1.39	-1.18	-1.29	8.04E-07	268878	Atp13a5	ATPase type 13A5
1452474_a_at	-1.43	-1.06	-1.24	9.85E-08	109979	Art3	ADP-ribosyltransferase 3
1448649_at	-1.35	-1.13	-1.24	1.13E-07	13809	Enpep	glutamyl aminopeptidase
1424254_at	-1.15	-1.29	-1.22	0.000503714	68713	Ifitm1	interferon induced transmembrane protein 1
1428538_s_at	-1.44	-0.86	-1.15	5.31E-05	71660	Rarres2	retinoic acid receptor responder (tazarotene induced) 2
1436134_at	-1.02	-1.21	-1.11	2.85E-05	72821	Scn2b	sodium channel, voltage-gated, type II, beta
1438288_x_at	-1.08	-1.06	-1.07	0.003920521	68786	1110059G02Rik	RIKEN cDNA 1110059G02 gene
1448443_at	-1.18	-0.89	-1.04	2.43E-06	20713	Serpini1	serine (or cysteine) peptidase inhibitor, clade I, member 1
1425505_at	-0.86	-1.20	-1.03	0.000253317	107589	Mylk	myosin, light polypeptide kinase
1426855_at	-1.15	-0.86	-1.01	0.000155467	52666	Arhgef25	Rho guanine nucleotide exchange factor (GEF) 25
1452670_at	-1.01	-0.97	-0.99	1.06E-06	98932	Myl9	myosin, light polypeptide 9, regulatory
1452308_a_at	-0.95	-0.96	-0.96	0.002749936	98660	Atp1a2	ATPase, Na+/K+ transporting, alpha 2 polypeptide
1452398_at	-1.04	-0.84	-0.94	6.64E-06	74055	Plce1	phospholipase C, epsilon 1
1450944_at	-1.01	-0.83	-0.92	7.53E-06	121021	Cspg4	chondroitin sulfate proteoglycan 4
1441881_x_at	-0.89	-0.94	-0.92	0.000169075	73121	Fam101a	family with sequence similarity 101, member A
1420871_at	-0.97	-0.86	-0.92	0.000298981	54195	Gucy1b3	guanylate cyclase 1, soluble, beta 3
1416287_at	-0.89	-0.94	-0.91	2.95E-06	19736	Rgs4	regulator of G-protein signaling 4
1449860_at	-0.97	-0.80	-0.88	1.32E-06	75689	Higd1b	HIG1 domain family, member 1B
1417012_at	-0.85	-0.90	-0.87	0.000917292	15529	Sdc2	syndecan 2
1418086_at	-0.94	-0.79	-0.86	2.73E-05	68458	Ppp1r14a	protein phosphatase 1, regulatory (inhibitor) subunit 14A
1416652_at	-0.90	-0.80	-0.85	1.19E-05	66695	Aspn	asporin
1424733_at	-0.94	-0.69	-0.82	3.61E-05	140795	P2ry14	purinergic receptor P2Y, G-protein coupled, 14
1455050_at	-0.95	-0.61	-0.78	3.31E-06	320736	Vstm4	V-set and transmembrane domain containing 4
1458341_x_at	-0.76	-0.75	-0.76	7.11E-07	242202	Pde5a	phosphodiesterase 5A, cGMP-specific
1423503_at	-0.76	-0.68	-0.72	6.34E-07	83964	Jam3	junction adhesion molecule 3
1426677_at	-0.71	-0.73	-0.72	1.64E-05	192176	Flna	filamin, alpha
1421096_at	-0.71	-0.68	-0.69	0.000426889	22063	Trpc1	transient receptor potential cation channel, subfamily C, member 1
1435254_at	-0.75	-0.62	-0.68	6.13E-07	235611	Plxnb1	plexin B1
1450757_at	-0.93	-0.43	-0.68	0.001176504	12552	Cdh11	cadherin 11
1422058_at	-0.69	-0.66	-0.68	0.000164929	18119	Nodal	nodal
1424768_at	-0.50	-0.80	-0.65	9.96E-05	109624	Cald1	caldesmon 1
1456885_at	-0.53	-0.77	-0.65	1.98E-05	20362	07-Sep	septin 8
1423104_at	-0.65	-0.64	-0.64	0.000273303	16367	Irs1	insulin receptor substrate 1
1428808_at	-0.67	-0.61	-0.64	3.03E-05	243548	Prickle2	prickle homolog 2 (Drosophila)
1440132_s_at	-0.80	-0.46	-0.63	6.72E-05	19085	Prkar1b	protein kinase, cAMP dependent regulatory, type I beta
1422510_at	-0.53	-0.73	-0.63	1.18E-05	69274	Ctdspl	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like
1444229_at	-0.43	-0.80	-0.61	0.013702059	11819	Nr2f2	nuclear receptor subfamily 2, group F, member 2
1417307_at	-0.67	-0.54	-0.61	5.51E-05	13405	Dmd	dystrophin, muscular dystrophy
1434647_at	-0.61	-0.57	-0.59	0.00043634	268780	Egflam	EGF-like, fibronectin type III and laminin G domains
1442143_at	-0.15	-1.01	-0.58	0.035152848	320091	Ano4	anoctamin 4
1435148_at	-0.73	-0.42	-0.57	7.97E-05	11932	Atp1b2	ATPase, Na+/K+ transporting, beta 2 polypeptide
1425102_a_at	-0.83	-0.30	-0.57	0.001486684	70008	Ace2	angiotensin I converting enzyme (peptidyl-dipeptidase A) 2
1420942_s_at	-0.46	-0.67	-0.56	0.000286771	19737	Rgs5	regulator of G-protein signaling 5
1439627_at	-0.59	-0.50	-0.55	0.000758294	22771	Zic1	zinc finger protein of the cerebellum 1
1417439_at	-0.65	-0.42	-0.53	0.000167586	70445	Cd248	CD248 antigen, endosialin
1416625_at	-0.72	-0.32	-0.52	0.00033911	12258	Serping1	serine (or cysteine) peptidase inhibitor, clade G, member 1
1425891_a_at	-0.71	-0.32	-0.51	0.000400968	66790	Grtp1	GH regulated TBC protein 1
1428250_at	-0.27	-0.58	-0.43	0.000168292	76854	Gpr30	G protein-coupled receptor 30
1419662_at	0.36	0.73	0.55	0.005804911	18295	Ogn	osteoglycin
1454974_at	0.46	0.67	0.57	0.036643268	18208	Ntn1	netrin 1
1434225_at	0.51	0.67	0.59	3.06E-05	20947	Swap70	SWA-70 protein
1460003_at	0.99	0.23	0.61	0.013396838	99132	AI956758	expressed sequence AI956758
1421817_at	0.61	0.65	0.63	0.006548341	14782	Gsr	glutathione reductase
1427883_a_at	0.71	0.82	0.77	0.000102634	12825	Col3a1	collagen, type III, alpha 1
1415871_at	0.68	0.92	0.80	0.000429412	21810	Tgfbi	transforming growth factor, beta induced
1436570_at	1.26	0.50	0.88	0.000664922	94212	Pag1	phosphoprotein associated with glycosphingolipid microdomains 1

References

1. Chi J-T, Rodriquez EH, Wang Z, Nuyten DSA, Mukherjee S, van de Rin M, Van de Vijver MJ, Hastie T, Brown PO. Gene expression programs of human smooth muscle cells: tissue-specific differentiation and prognostic significance in breast cancers. *PLoS Genet*. 2007;3:1770-84.

Supplemental Methods and Material

Mice

Notch3$^{-/-}$ (C57BL/6J) mice [1] were bred at the Karolinska Institute, K. M. Wallenberg Animal facility (Stockholm, Sweden). NG2DsRed BAC transgenic mice were obtained from Jackson Laboratories (stock 008241) and Notch3; NG2DsRED mice were bred at Uppsala University (Uppsala, Sweden). All mice were sex matched to their littermate controls and experiments were performed at 6-8 months of age unless otherwise stated. Animal experiments were approved by the Stockholm's North and Uppsala Ethical Committees for Animal Research.

Antibodies and immunohistochemistry

Mice were anesthetized and transcardially perfused with Hanks buffered salt solution (HBSS) containing 5 U/ml heparin, followed by a solution of 4% formaldehyde in phosphate buffered saline (PBS). Tissues were post fixed in 4% formaldehyde for 4 hours at 4°C. Immunohistochemistry was carried out on whole isolated retinas, and on vibratome brain coronal sections (30 or 50 μm) as described previously [2]. Briefly, tissues were blocked and permeabilized in PBS containing 1% bovine serum albumin and 0.5% TritonX-100 in PBS overnight at 4°C. Tissues were then incubated in primary antibody solution, washed, and subsequently incubated in secondary antibody solution. Each step was carried out overnight at 4°C. Sections were mounted in Prolong Gold Antifade reagent with DAPI (cat. # P36931; Invitrogen). The following primary antibodies were used: mouse anti-human α-smooth muscle actin (Cy3 conjugated - cat. # C6198, FITC conjugated - cat. # F3777, Sigma Aldrich); rat anti-mouse CD31 (cat. # 553370, BD PharMingen); goat anti-CD13 (cat. # AF2335, R&D Systems); rabbit anti-fibrinogen (cat. # A0080, DAKO); rabbit anti-β-gal (Cappel; cat. # 55976, MP Biomedicals); rabbit anti-iba1 (cat. #019-19741, WAKO); rat anti-GFAP directly conjugated to Cy3 (cat. # C9205, Sigma); rabbit anti-desmin (cat. # ab15200-1, Abcam); rabbit anti-NG2 (cat. # ab5320, Millipore). rabbit anti-cleaved caspase 3 (cat. # 9661, Cell Signaling); rabbit anti-Claudin-5 (cat. # 34-1600, Zymed labs); rabbit anti-ZO-1 (cat. # 402200, Invitrogen); rabbit anti-Occludin (cat. # 71-1500, Zymed labs). Specimens were analyzed using LSM 510 META (Carl Zeiss AG), Axioplan 2 (Carl Zeiss AG) or Eclipse E800 (Nikon Instruments Europe B.V.) microscope. Image analysis was carried out using Image J (NIH), Volocity (Perkin Elmer) and Adobe image suite software.

Analysis of vasculature of NG2DsRED, *Notch3*$^{-/-}$ animals

Mice were anesthetized and transcardially perfused with HBSS followed by 4% formaldehyde in PBS. Brains were removed and images were captured using an M205 FA (Leica) stereomicroscope equipped with a DFC450-C (Leica) camera.

Blood-brain barrier integrity studies using exogenous tracers

The following tracers were used: Evans blue (2% in PBS, 80 μl/20 g, intraperitoneal administration; Sigma Aldrich), 70 kDa dextran conjugated to tetramethylrhodamine (TMR) (25 mg/ml, 2 mg/20 g, intravenous administration; Invitrogen), horseradish peroxidase (100 mg/ml, 10 mg/20 g; Sigma Aldrich). Evans blue and 70 kDa dextran-TMR were circulating for 16 hours, and horseradish peroxidase for 10 minutes. Evans blue in the brain was quantified by spectrophotometry as described [3]. For *in situ* detection of injected tracers, anesthetized animals were transcardially perfused for 5 minutes with HBSS, followed by a 5 minute perfusion with 4% formaldehyde in PBS, pH 7.2. Horseradish peroxidase was visualized using the 3,3´-diaminobenzidine tetrachloride/nickel-cobalt kit (cat. #00-2013, Invitrogen) according to the manufacturer's instructions. Samples were analyzed using LSM 510 META (Carl Zeiss AG) and Eclipse E800 (Nikon Instruments Europe B.V.) microscopes.

Quantitation of mural cell coverage

Pericytes: Quantification of pericytes was carried out in 1 retina from 3 adult (6-8 months old) mice per genotype, which were stained for CD13 pericyte marker, β-gal, and CD31 to stain endothelial cells. Images were taken of both the superficial and deep capillary plexuses for each retina. All pericytes in each image, positive for CD13 and β-gal expression, were counted. Total capillary length was measured in each image using Image J (NIH) software.

Vascular smooth muscle cells: Whole retinas were stained for SMA, and CD31 as a vessel costain. 100x magnification images were taken on an Axioplan 2 (Carl Zeiss AG) microscope then stitched and blended together using Adobe Photoshop CS6 automatic image merge function. A grid was placed over the composite image to indicate the perimeter of three zones; 820, 1640 and 2710 μm from the origin of the optic nerve. Three primary radial arterioles were measured in 1 retina from 4 animals per genotype, using Image J (NIH) software. A gap in SMA coverage was defined as an area showing no detectable SMA staining around the entire circumference of the artery. Each gap was then measured until the point of clear coverage of SMA expression around the entire circumference.

Quantitation of β-gal expression in gaps

One primary retinal arteriole from each of three *Notch3*$^{-/-}$ mice was imaged along its length at 400x magnification on an LSM META 510 confocal microscope (Carl Zeiss AG). A gap was defined as above and a minimum gap length of 20 μm was applied to ensure no contact between neighboring cells. The presence or absence of β-gal expression in each gap was determined by an independent observer.

Quantitation of GFAP coverage of retinal vasculature

Two primary retinal arterioles and one venule from each of three *Notch3*$^{-/-}$ and *Notch3*$^{+/-}$ mice was imaged from the origin of the optic nerve at 100-200x magnification on an Axioplan 2 (Carl Zeiss AG) microscope. Images of GFAP staining were converted to 8-bit greyscale in Image J (NIH) and subjected to automatic threshold using the Li method. Regions of interest were drawn around the length of each vessel (See Supplemental Figure XI) and % threshold value used as quantitation of the % astrocyte coverage.

Quantitation of cleaved caspase 3 positive cells in retinal vasculature

Quantitation was carried out in one retina from three mice per genotype. Cleaved caspase 3 positive cells and branches were counted along the first 1200 mm of three primary radial arterioles, beginning at the origin of the optic nerve.

Electron microscopy

Three 12-month-old *Notch3*$^{-/-}$ mice and three *Notch3*$^{+/-}$ littermate controls were anaesthetized and transcardially perfused with HBSS followed by fixative (2% formaldehyde, 2.5% glutaraldehyde, and 0.02% Na azide, in 0.05 M Na cacodylate buffer, pH 7.2). Eyes were removed and whole retinas were collected by microdissection. The retinas were cut from the anterior rim with fine scissors into a flower-like shape with 4-6 triangular petals held together at the optic disc region, and were further fixed for 24 h. Post-fixation was performed with 1% osmium tetroxide + 1% K hexacyano-ferrate in 0.1 M cacodylate. After *en bloc* contrasting with 0.5% uranyl acetate, dehydration and epoxide resin (Agar 100) infiltration followed according to laboratory routines. Once in the final plastic, individual "flower petals" of the retinas were forced by applied pressure to a flattened shape between Aclar films, and allowed to cure by heat. Gelatine capsules with pre-polymerized plastic were mounted to the pigment

layer aspect of the thin samples. A serial sectioning with a diamond histo-knife (Diatome, Biel, CH) was done at 1 μm microtome setting from the inner aspect of the flattened retinas. Repeatedly, sections were collected and stained (Richardson's stain) for light microscopic evaluation. When longitudinally cut vessels were encountered, that specific area was trimmed for ultrathin sectioning with a Leica UC6 ultramicrotome (Leica Microsystems, Vienna, AU) fitted with a diamond EM knife (Diatome) at 50-60 nm thickness. Sections were collected on copper grids and contrasted with uranyl acetate and lead citrate. They were examined in a LEO 912 AB Gemini TEM (Carl Zeiss NTS, Oberkochen, DE) with a LaB_6 emitter operated at 120 kV. Digital imaging (2x2 kpixel) was made with a Veleta CCD camera (Olympus-SiS, Münster, DE). Microscope and camera were run under the iTEM software (Olympus-SiS).

Purification of brain microvasculature

Purification of microvasculature from *Notch3*$^{-/-}$ and littermate *Notch3*$^{+/+}$ control mice (n = 3, age 2 months) was carried out as described [4]. Two samples (cerebral and cerebellar regions) from each mouse were collected, purified and analyzed separately. 12 samples in total. Briefly, brain tissue was digested using Collagenase A for 15 minutes at 37^{o}C. The resulting tissue digest was filtered through 100 μm and subsequently through 40 μm cell strainer. Microvessels were captured using rat anti-CD31 coated Dynabeds. Isolated microvessels were lysed in a lysis buffer for RNA extraction. RNA was purified using RNA isolation kit from Qiagen. Isolated microvessels contain endothelial cells, pericytes, and vessel associated astrocytes.

Transcription profiling and bioinformatics analysis

Total RNA was extracted from cerebral and cerebellar microvascular fragments from three mice per genotype (as described above) and hybridized separately to Mouse Genome 430 2.0 Arrays according to standard procedures outlined by the manufacturer (Affymetrix, Santa Clara, CA, USA). 12 arrays were used in total. Affymetrix raw data were normalized using Bioconductor GCRMA package (Bioconductor gcrma package, version 2.32.0) in R software (www.r-project.org, *R version 3.0.1*). The R function used for normalization was just.gcrma(filenames=[CEL_file_list], type=c("fullmodel"), optimize.by=c("memory")), and then function "exprs" was used to retrieve the entire normalized data into a gene expression matrix table. To identify the differentially expressed genes between *Notch3*$^{-/-}$ tissues and controls, and also between cerebral and cerebellar vasculature, two way ANOVA analysis was performed. For this, R function anova with standard settings was used, and the genotype and brain region were the two variables. Genes which showed a P value <0.05 and fold change >1.5 (log2 fold 0.58) in either comparison were considered significant. The entire microarray data set has been deposited in the NCBI Gene Expression Omnibus database (www.ncbi.nlm.nih.gov/geo/, accession number GSE55203). *Pdgfb*$^{ret/ret}$ transcriptome data published previously [2] were compared with the *Notch3* data obtained in this study.

Statistical analysis

Statistical significance was determined by using unpaired two-tailed Student's t-test (GraphPad Prism5). Differences were considered significant with a P value <0.05. Quantified data are presented as mean +/- standard deviation (s.d.) or standard error of the mean (s.e.m) as indicated.

References

1. Mitchell KJ, Pinson KI, Kelly OG, Brennan J, Zupicich J, Scherz P, Leighton PA, Goodrich LV, Lu X, Avery BJ, Tate P, Dill K, Pangilinan E, Wakenight P, Tessier-Lavigne M, Skarnes WC. Functional analysis of secreted and transmembrane proteins critical to mouse development. *Nat Genet*. 2001;28:241–9.

2. Armulik A, Genové G, Mäe M, Nisancioglu MH, Wallgard E, Niaudet C, He L, Norlin J, Lindblom P, Strittmatter K, Johansson BR, Betsholtz C. Pericytes regulate the blood-brain barrier. *Nature*. 2010;468:557–61.

3. Su EJ, Fredriksson L, Geyer M, Folestad E, Cale J, Andrae J, Gao Y, Pietras K, Mann K, Yepes M, Strickland DK, Betsholtz C, Eriksson U, Lawrence DA. Activation of PDGF-CC by tissue plasminogen activator impairs blood-brain barrier integrity during ischemic stroke. *Nat Med*. 2008;14:731–7.

4. Wallgard E, Larsson E, He L, Hellström M, Armulik A, Nisancioglu MH, Genove G, Lindahl P, Betsholtz C. Identification of a core set of 58 gene transcripts with broad and specific expression in the microvasculature. *Arterioscler Thromb Vasc Biol*. 2008;28:1469–76.